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AF047416 MUS muscu
AF029753 MUS muscu
AF03525 MUS muscu
AF036945 MUS muscu
AF036945 MUS muscu
AF036945 MUS muscu
AF036945 MUS muscu
AF0369718 Homo sapi
AC115183 Rattus no
BK932800 Gallus ga
AF047419 Homo sapi
AF060871 Kenopus 1
AF060871 Homo sapi
AF087036 Homo sapi
AF0608318 Homo sapi
AC115876 MUS muscu
AC115876 MUS muscu
AC115876 MUS muscu
AC121789 MUS muscu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AB094420 Sus scrof
AC141743 Apis mell
CQ530499 Sequence
BV184299 sqnm14420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CR450293 537 bp mRNA linear PRI 18-MAY-2004 Homo sapiens full open reading frame cDNA clone RZPDo834B111D for gene TCF21, transcription factor 21; complete cds; without
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Bases 1 to 53)

Cloning of human full open reading frames in Gateway(TM) system entry vector (pDONR201)

Unpublished

2 (bases 1 to 537)

Ebert, L., Schick, M., Neubert, P., Schatten, R., Henze, S. and Korn, B. Direct Submission

2 (bases 1 to 537)

Ebert, L., Schick, M., Neubert, P., Schatten, R., Henze, S. and Korn, B. Direct Submission

Submitted (18-MA-2004) RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH, Im Neuenheimer Feld 580, D-69120 Heidelberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Germany
KZPD; RZPDc834B111D, ORFNo 76
www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPDo834B111D RZPDLIB;
Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD LIB No.
834
AL356109 Human DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CR450293.1 GI:47496532
Full ORF shuttle clone, Gateway(TM), complete cds.
Homo sapiens (human)
Homo sapiens
                AF047418
AF029753
AF029753
AF02525
AF035718
AF035718
AF035718
AF011282
AF047419
BF047419
BF047419
BF047419
BF047419
BF047419
BF047419
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BF047419
BF061782
BF061782
BF061782
BF06184
AF18876
AF087035
AF0870
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43.0 124070
43.0 231207
37.4 189465
34.1 697
20.1 240
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170668
181157
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225399
222122
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KEYWORDS
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AUTHORS
TITLE
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REFERENCE
AUTHORS
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JOURNAL
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CR450293
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BD211771 Proteins
BC025697 Homo sapi
CQ718038 Sequence
                                                                                                                       December 17, 2004, 00:05:37 ; Search time 3793 Seconds (without alignments) 2231.705 Million cell updates/sec
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tter than or equal to the score of the result being printed,
ived by analysis of the total score distribution.
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179
1 MSTGSLSDVEDLQEVEMLEC......PESDLKEVVTASRLCGTTAS 179
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                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                         OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                       4526729 segs, 23644849745 residues
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7.0
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BD211771
BC025697
CQ718038
                                                                                                                                                                                                                                                                                   Xgapop 60.0 , Xgapext
Ygapop 60.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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1: gD ba: *
2: gD htg: *
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: gD ov: *
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: gD pl: *
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Maximum DB seq length: 200000000
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and is derived by a
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Euter (10.1272)
Euter (10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAT 17-JUL-2003
                                                                                                                                                            121 LeuArgLeuAlaSerSerTyrIleAlaHisLeuArgGlnIleLeuAlaAsnAspLysTyr 140
                                                                                                                                                                                                                                                                                                             GluAsnGlyTyrIleHisProValAsnLeuThrTrpProPheMetValAlaGlyLysPro 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bandman, O., Corley, N.C., Patterson, C. and Lu, D.A.M.
                                                                                        360
                                                                                                                                                                                                                                                                                                                                                                  421 GAGAACGGGTACATTCACCCGGTCAACCTGACGTGGCCCTTTATGGTGGCCGGGAAACCC 480
                                                                                                                                                                                                                                 361 CTCAGGCTGGCGTCCAGCTACATCGCCCACTTGAGGCAGATCCTGGCTAACGACAAATAC 420
                ArgLeuLysThrThrLeuProTrpValProProAspThrLysLeuSerLysLeuAspThr 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          268 ATGTCCACCGGCTCCCTCAGCGATGTGGAGGACCTTCAAGAGGTGGAGATGTTGGAATGT 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-OCT-1998 US 60/104624
PI PRETET LAL, HENRY YUE, Y TOM TANG, JENNIFER L HILLMAN, OLGA PI BANDMAN,
PI NELL C CORLERY, KARL J GUEGLER, GINA A GORGONE, MARIAH R BAUGHN,
PI CHANDRA PATTERSON, DYUNG ALNA M LU
PC C12N15/00, A61828/00, A61829/395, A61829/395, A61845/00, A61825/00,
PC A61825/00, A61827/02, A61843/00, C07814/47, C07816/18, C12N15/00, PC A61825/00, A61827/02, A61829/395, A61829/395, A61825/00, PC A61829/395, A61829/395, A61829/395, A61825/00, PC A61829/395, A61829/395, A61825/00, PC A61829/395, A61825/00, PC A61829/395, A61829/395, A61825/00, PC A61829/395, A61825/00, PC A61829/395, A61829/395, A61825/00, PC A61829/395, A61829/395, A61825/00, PC A61829/395, A61829/395, A61825/00, PC A61829/395, A61825/00, A61825/00, A61829/395, A61825/00, A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ద
                                                    301 AGACTCAAGACCACCCTGCCCTGGGTGCCCCCGGAAGCTCTCCAAGCTGCAGGACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  161 GluSerAspLeuLysGluValValThrAlaSerArgLeuCysGlyThrThrAlaSer 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MetSerThrGlySerLeuSerAspValGluAspLeuGlnGluValGluMetLeuGluCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              481 GAGAGTGACCTGAAAGAAGTGGTGACCCCGCATATGTGGGAACCACCGCGTCC
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Matches:
Conservative:
Mismatches:
Indels:
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BD211771
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Homo sapiens (human)
Homo sapiens
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Best Local Similarity:
Query Match:
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Pred. No.:
                101
                                                                                                                                                                                                                                                                                                                     141
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ACCESSION
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BD211771
LOCUS
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                                                                                                                                                                                                                                                                                                     This clone is available from RZPD;
contact RZPD (customer.service@rzpd.de) for further information.
This CDS clone is a part of a collection of human full length
expression clones generated by RZPD.
This CDS has been cloned without stopcodon.
The CDS has been inserted into pDONR201 via a BP Clonase(TM)
reaction. Additional sequence has been added in front of the start
codon (ATG): att. AAAAA GCT GGC ACC CCT GGT CCA GGT (RAG)
After the last codon additional sequence has been added: CCA GGC
CCA GGC Gin front of the 3' att site (AC CCA GGT TTC TT).
Compared to the reference sequence NM_003206 we did not find any
amino acid exchanges.
Clone distribution: http://www.rzpd.de/products/orfclones/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="TCF21"
/codon start=1
/protein_id="CAG29289.1"
/db_xxef="G1:47486533"
/translation="MNTGSLSDVEDLQBVEMLECDGLKMDSNKEFVTSNESTEESSNC
RANSPOKGRGGKRRKAPTKKSPLSGVSQEGKQVQRNAANARERARNKVLSKAFSRL
KTTLPWVPPDTKLSKLDTLRASSYIAHLRQILANDKYENGYIHPVNLTWPFWVAGKP
ESDLKEVVTASRLCGTTAS."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 CGCAACGCCGCCAACGCGCGAGAGCGGGCCCGCATGCGAGTGCTGAGCAAGGCCTTCTCC 300
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www.rzpd.de/cgi-bin/products/showLib.pl.cgi/response?libNo=834
www.rzpd.de/products/orfolones/
Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH,
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Pax: +49 30 32639 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
/db xref="taxon:9606"
/clone="RZPD08348111D"
/clone lib="Human Full ORF Clones Gateway(TM) - RZPD"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pDONR201, Site_1: attP1; Site_2: attP2"
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Mismatches:
Indels:
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Matches:
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/gene="TCF21"
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Best Local Similarity:
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Calthersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mg-ompail.nih.gov/
Contact: nisc_mg-ompail.nih.gov/
Contact: nisc_mg-ompail.nih.gov/
Contact: nisc_mg-ompail.nih.gov
Blakesley,R.W., Agele,K., Bestrom-Sternberg,S.W., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Grannite,S., Guan,X., Gupta,J., Haghighi,P.,
Dietrich,N.H., Ho.S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /trānslation="MSTGSLSDVBDLOEVEMLECDGLKMDSNKEFVTSNESTEESSNC
STOLEGPOKAGGGGKRRKAPTKKSPLSGVSOEGKOVORNAANREERARNKVLSKAFSRL
KTTLPWVPPDTKLSKLDTLRLASSYIAHLRQILANDKYENGYIHPVNLTWPFMVAGKP
ESDLKEVVTARRLGGTTAS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SerSerAsnCysGluAsnGlySerProGlnLysGlyArgGlyGlyLeuGlyLysArgArg 60
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NIH-WGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: gapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.B. Consortium (LINL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="transcription factor 21"
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Matches:
Conservative:
Mismatches:
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260. 799
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Strausherg R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Scheefer (C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.L., Wang, J., Hsieh, F.,

Diatchenko, L., Maruslana, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleron, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulk, S.W.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, B., Ketteman, M., Madan, A., Rodriques, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Schmutz, J., Myers, R.M.,

Butterfield, A.S., Schein, J.B., Jones, S.J. and Marra, M.A.,

Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BC025697 3231 bp mRNA linear PRI 30-JUN-2004 Homo sapiens transcription factor 21, transcript variant 1, mRNA (CDNA clone MGC:34534 IMAGE:5221575), complete cds.
                                                                                                                                         447
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  ArgAsnAlaAlaAsnAlaArgGluArgAlaArgMetArgValLeuSerLysAlaPheSer 100
                                                                                                                                                                                                                                                                                                                                                                                                            ArgleulysThrThrLeuProTrpValProProAspThrLysLeuSerLysLeuAspThr 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LeuArgleuAlaSerSerTyrIleAlaHisLeuArgGlnIleLeuAlaAsnAspLysTyr 140
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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3231)
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Submitted (06-MAR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GluSerAspLeuLysGluValValThrAlaSerArgLeuCysGlyThrThrAlaSer 179
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                                                                                                                                                                                            LysAlaProThrLysLysSerProLeuSerGlyValSerGlnGluGlyLysGlnValGln
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                                                                                                                   AGCTCCAACTGCGAGAATGGGTCTCCCCAGAAGGGCCGCGGGGGCCTGGGCAAGAAGGAGG
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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AUTHORS
TITLE
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AUTHORS
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BC025697
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/product=104337410.1 (transcription factor 21)"
/protein_id="CAC26822.1"
/protein_id="CAC26822.1"
/db_xref="CAC3680"
/db_xref="CAC3.043680"
/db_xref="CAC3.04368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18737. 18828.

Incre="18 copies 2 mer ct 97% conserved"
19018-"19133 repeat: matches 1. .121 of consensus"

/noce="match: STS: Em:G21594"

complement(19114. .19339)
/noce="match: STS: Em:G1594"

complement(19114. .19339)
/noce="match: STS: Em:G14783"
20263. .20325
/noce="L2 repeat: matches 2675. .2750 of consensus"
20892. .21097
/noce="klussy repeat: matches 1. .207 of consensus"
2164. .21277
/noce="MRR21B repeat: matches 7. .128 of consensus"
21279. .23359
/noce="MRR21B repeat: matches 274. .361 of consensus"
21279. .23359
/noce="MRR21B repeat: matches 274. .361 of consensus"
21279. .23359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            // ince="MEEZIS" repeat: matches 324. .714 of consensus" complement(21885. .22328) / ince="match: GSS: Em:AQ416499" complement(21975. .22377) / ince="match: GSS: Em:AQ005575" / ince="match: GSS: Em:AQ005575" / ince="match: GSS: Em:AQ005575"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23399. .23661
/note="MLT1H repeat: matches 285. .547 of consensus"
23662. .23960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="AluJb repeat: matches 1. .301 of consensus" 23961. .24243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2898. .z.susa
note="MIR repeat: matches 60. .212 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .156 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="match: GSS: Em:AL212694 Em:AL254874"
complement(13513. .13636)
/note="match: GSS: Em:AL214858"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8016. .18073 
note="29 copies 2 mer ct 72% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /evidence-not_experimental
complement(15683. 16091)
/note-=match: 6Ss: Em:AQ031468"
complement(15788. 16037)
/note="match: STS: Em:G15194"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    match: STS: Em:G48886"
complement(22530. .23061)
/note="match: GSS: Em:AQ792775"
22898. .23051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="match: GSS: Em:AQ486523"
22364. .22813
note="match: GSS: Em:B82669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7643. .17736
note="MIR repeat: matches 49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       evidence=not_experimental 3326. .13636
gene="TCF21"
                                                                                                                                                                                                                                                                                                                                                                                                                                          note="CpG island"
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/ yetter = 1.0.74.1. (branscription factor 21)"
/ note="match: cDNAs: Em.AB009453 Em.AF036945 Em:AF029753
Em.AF087036 Em.AF047418 Em.AF035718 Em.AF0419
Em.AF087036 Em.AF06154 Em.AF108216 Em:M99367 Em:AF061752
Em:AF007595 Em.L35922 Em.AF109012 Em:M96923 Em:Y09596
Em:M007595 Em:1018658
Em:AF1087231 Em:AM313610 Em:W78859 Em:AA880760 Em:AY027658
Em:AA22648 Em.AM313610 Em:W78859 Em:AA380760 Em:AY02566
Em:AM32703 Em.AM33365 Em:AM432075 Em:AA380760 Em:AA028184
Em:AA02703 Em.AM583915 Em:AM78678 Em:AA028032
Em:AA02703 Em.AA33365 Em:AA170804 Em:AA18693
Em:AA38622 Em:AA33366 Em:AA170604 Em:AA18693
Em:AA38622 Em:AA331062 Em:AA1721064 Em:AA36142 Em:AA36354
Em:AA38620 Em:AA381062 Em:AA31062 Em:AA341736
Em:AA319336 Em:AA985950 Em:AA341736
Em:AA319336 Em:AA985950 Em:AA341730 Em:AA341730 Em:AA341730 Em:AA341730 Em:AA341730 Em:AA341730 Em:AA341730 Em:AA341730 Em:AA341730 Em:AA340993 Em:AA351557
Em.AA319336 Em:AA91130 Em:H51772 Em:AA340993 Em:AV351557
                                                                                                                                                                                                                /clone="RP11-373A10"
/clone_lib="RPC1-11.2"
376. -743
/note="LiMB7 repeat: matches 5789. .6171 of consensus"
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700ce="MLTIJ repeat: matches 325. .487 of consensus"
7277. .6407
7note="12 repeat: matches 2554. .2749 of consensus"
                                                                                                                                                                                                                                                                                                                                            2126. .2147
Note="11 copies 2 mer aa 100% conserved"
896. .3155
Note="AluJo repeat: matches 36. .295 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .2509 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4530. .4942
/note="MLT1B repeat: matches 3. .386 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7111. .7210

Anote="MIR repeat: matches 155. .259 of consensus"

7253. .7703

Anote="L2 repeat: matches 1969. .2509 of consensus'

401. .9688

Anote="AluSg repeat: matches 1. .298 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .271 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5481. .6770
/note="MLT1F repeat: matches 1. .264 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .255 of consensus"
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Ancte="14 copies 2 mer ac 100% conserved"

1922. 16041

Gene="TCF21"

join(12922. 13631,15497. 16041)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              join(12922. .13631,15497. .16041)
/gene="TCF21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1979. .5249
/note="AluJo repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat: matches 28.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              367. .6702
note="match: GSS: Em:B31477"
                                                                 .. .25186
'organism="Homo sapiens"
                                                                                                                        /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/chromosome="6"
VECTOR: pBACe3.6.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                              3472. .3680
/note="MIR repeat: π
4173. .4656
/note="match: GSS: Ε
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AF029753.1 GI:2613018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   561
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      322 TCCAACTGCGAGAACGGGTCTCCACAGAAGGGTCGCGGTGGCCTAGGCAAGAGGGGGAAG 381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81
                                                                                                                                                                                                          199. .738
/function="basic helix-loop-helix transcription factor"
PO Royal Melbourne Hospital
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ArgleuAlaSerSerTyrIleAlaHisLeuArgGlnIleLeuAlaAsnAspLysTyrGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SerAsnCysGluAsnGlySerProGlnLysGlyArgGlyGlyLeuGlyLysArgArgLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 AlaproThrLysLysSerProLeuSerGlyValSerGlnGluGlyLysGlnValGlnArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCGCCCACTAAGAAAAGCCCGCTCAGCGGGGTCAGCCAGGAGGGCAAGCAGGTCCAGCGC
                                                                                                                                                                                                                                                  /note="expressed in embryonic epicardium and mesenchyme-derived tissues of lung, gut, kidney, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1202
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Conservative:
Mismatches:
Indels:
Hall Institute of Medical Research,
Melbourne, VIC 3050, Australia
Location/Qualifiers
1. .1202
                                                                                         /organism="Mus musculus"
/mol type="mRNA"
strain="Balb/c"
/db_xref="taxon:10090"
199. 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-701-674A-23 (1-179) x AF047418 (1-1202)
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Mus musculus
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100.00%
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67.04%
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Best Local Similarity:
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DB:
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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Robb,L., Mifsud,L., Hartley,L., Biben,C., Copeland,N.G., Glibert,D.J., Jenkins,N.A. and Harvey,R.P. epicardin. A noohkins,N.A. and Harvey,R.P. expressed in epicardin. branchial arch myoblasts, and mesenchyme of developing lung, gut, kidney, and gonads
Dev. Dyn. 213 (1), 105-113 (1998)
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Robb.L. and Mifsud.L.
Direct Submission
Submitted (10-FEB-1998) Haematology and Cancer, Walter and Eliza
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Mus musculus epicardin mRNA, complete cds.
AF047418
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Matches:
Conservative:
Mismatches:
Indels:
13602 GAGAACGGGTACATTCACCCGGTCAACCTG 13631
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Best Local Similarity:
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Mus musculus
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                                                                                                                                                                                                                                                                                    /codon_start=1 /product == basic helix-loop-helix factor Corl" /protein_id="hasic helix-loop-helix factor Corl" /protein_id="hasic helix-loop-helix factor Corl" /protein_id="hase4256.1" /db.xref="fd:s2613019" /translation="WSTGSLSDVEDLQEVENLDCDSLKVDSNKEFGTSNESTEEGSNC ROSSPGKGGLGKRRKAPTKKSPLSGVSQECKQVQRNAANARERAARRVLSKAFSRL KTTLPWVPPDTKLSKLDTLALASSYIAHLRQILANDKYENGYIHPVNLTWPFWVAGKP ENDLKEVVTANRLCGTTAS"
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                                             2 (bases 1 to 1217)
Quertermous, T., Quertermous, E.E., Hidai, H., Fadel, B., Boutet, S.C.
and Bardales, R.
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Submitted (10-OCT-1997) Department of Medicine, Division of
Cardiology, Stanford University, Falk Bldg, 300 Pasteur Drive,
Stanford, CA 94305, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                   1217
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Matches:
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/organism="Mus musculus"
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nephgonadin.
Mus musculus (house mouse)
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Mus musculus mRNA for
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/creatism="Mus musculus"
/mol_type="mRNA"
/do_xref="taxon:10090"
223...762
223...762
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/mottion="transcription factor"
/note="basic helix-loop-helix gene"
/codon start=1
/creati_id="paA23883.1"
/producl="nephgonadin"
/producl="mSPA23883.1"
/do xref="GI:2696118"
/translation="MSTGSLSDVEDLQEVEMLDCDSLKVDSNKEFGTSNESTEGSNC
ENGSPGGRGGGRRRKAPTKKSPLSGVSQEGKQVQRNAANARERGTSNESTEGSNC
ENGSPGGGGGGRRRKAPTRKSPLSGVSQEGKQVQRNAANARERGTSNESTEGSNC
ENGSPGGGGGGRRRKAPTRKSPLSGVSQEGKQVQRNAANARERARMRVLSKAPSRL
KTTLPWVPPDTKLSKLDTLELASSYTAHLRQILANDKYENGYIHPVNLTWPFMVAGKP
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Mammalia; Butharia; Rodentia; Sciurognathi; Muridae; Buteleostomi; Mammalia; Butharia; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1220)
Tamura,M. and Nakatsuji,N.
Identification of Nephgonadin, a novel basic helix-loop-helix gene published only in DataBase (1997)
2 (bases 1 to 1220)
Tamura,M. and Nakatsuji,N.
Direct Submission
Submitted (04-DEC-1997) Masaru Tamura, National Institute of Genetics, Mammalian Development; Yata 1111, Mishima, Shizuoka 411, Japan (E-mail:matamura@lab.nig.ac.jp, Tel:+81-559-81-6832,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ArgLeuAlaSerSerTyrIleAlaHisLeuArgGlnIleLeuAlaAsnAspLysTyrGlu 141
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Matches:
Conservative:
Mismatches:
Indels:
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/note="17 A nucleotides"
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                                                                                                                                                                                                                                                                                       Fax:+81-559-81-6828)
Location/Qualifiers
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Best Local Similarity:
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161

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eukheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (Dases 1 to 1246)

Rammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Alaschul, S.F., Zeeberg, B. Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Abramson, R.D., Mullahy, S.J., Boask, S.A., McEwan, P.J., Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodersen, P.H., Richards, S.W., Villalon, D.K., Muzny, D.M., Sodersen, R.D., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmitz, J., Myers, R.M., Butterfileld, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M. A., Non, S. Jone, Marla, M. A., Man A., Man A., Man A., Man A., Man A., Man, M. Socheration and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WITH-MGC Project 'URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: ogapba-ramail.nih.gov
Tissue Procurement: Jeffrey B. Green, M.D.
CDNA Library Prayade by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Galthersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Backstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Vonne, A., And C., Malker,M., Wetherby,K.D., Wiggins,L.,
Vonne, A., And C., Wiggins,L., Wetherby, M., Wetherby, W., Wet
                                                                                                                                                                                                                                                                      ncussess
Mus musculus transcription factor 21, mRNA (cDNA clone MGC:58914
MAGE:6529241), complete cds.
589 AGGCTGGCGTCCAGCTACATTAAGGCAGATCCTGGCCAACGACAAGTACGAG 648
                                                                                                                                                                    649 AACGGTTACATTCACCCAGTCAACCTGACGTGGCCCTTTATGGTGGCCGGCAAACCAGAG 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 108 Row: p Column: 16. Location/Qualifiers
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Submitted (09-UN-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                         142 AsnGlyTyrIleHisProValAsnLeuThrTrpProPheMetValAlaGlyLysProGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (house mouse)
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BC053525.1 GI:31566109
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Strausberg, R.
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VERSION
KEYWORDS
SOURCE
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AUTHORS
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TITLE
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COMMENT
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                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 1240)
Quaggin, S.E., Vanden Heuvel, G.B. and Igarashi, P.
Pod-1, a mesoderm specific basic-helix-loop-helix protein expressed in mesenchymal and glomerular epithelial cells in the developing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tränslation="MSTGSLSDVEDLQEVEMLDCDSLKVDSNKEFGTSNESTEEGSNC
ENGSPQKGRGGLGKRRKAPTKKSPLSGVSQEGKQVQRNAANARERARNRVLSKAFSRL
KTTLPWVPPDTKLSKLDTLRLASSYIAHLRQILANDKYENGYIHPVNLTWPFMVAGKP
ENDLKEVVTANRLCGTTAS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LeuLysThrThrLeuProTrpValProProAspThrLysLeuSerLysLeuAspThrLeu 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 ArgLeuAlaSerSerTyrIleAlaHisLeuArgGlnIleLeuAlaAsnAspLysTyrGlu 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 1240)
Quaggin, S.B., Vanden Heuvel, G.B. and Igarashi, P.
Direct Submission
Submitted (24-NOV-1997) Internal Medicine, Yale University, 333
Cedar Street, New Haven, CT 06520-8029, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SerAsnCysGluAsnGlySerProGlnLysGlyArgGlyGlyLeuGlyLysArgArgLys
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/product="mesoderm-specific basic-helix-loop-helix
                                                                                                                                                                                                                                                                                                                                                                                                            162 (a)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         457. .618
/gene="Pod1"
/note="encodes basic-helix-loop-helix domain"
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Mismatches:
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
mol type="mRNA"
db_xref="taxon:10090"
/chromosome="10"
/map="near DloMit2"
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/db_xref="GI:2745885"
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                                                                                                     Mus musculus (house mouse)
Mus musculus
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/gene="Pod1"
/note="Pod-1"
                                          GI:2745884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.17e-120
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226. .765
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1254 bp mRNA linear PRI 05-OCT-1998 Homo mapiens mesoderm-specific basic-helix-loop-helix protein (PODI) mRNA, complete cds. AF035718 AF035718 1 GI:2745RRA
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/db_xref="G1:269595"

                                                                                     epicardial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 ArgLeuAlaSerSerTyrIleAlaHisLeuArgGlnIleLeuAlaAsnAspLysTyrGlu 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      387 TCCAACTGCGAGAACGGGTCTGCACAGAAGGGTCGCGGTGGCCTAGGCAAGAGGAAG 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         447 GCGCCCACTAAGAAAGCCCGCTCAGCGGGGTCAGCCAGGAGGCAAGCAGGTCCAGCGC 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                627 Aggerigacerceaerracarcecreaerraaggeagarcergaceaacgacaagracaag 686
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 1267)
Lu, J., Richardson, J.A. and Olson, E.N.
capsulin: a novel bHLM transcription factor expressed in epicardia progenitors and mesenchyme of visceral organs
Mech. Dev. 73 (1), 23-32 (1998)
Mor. 10 2 (4)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42 SerAsnCysGluAsnGlySerProGlnLysGlyArgGlyGlyLeuGlyLysArgArgLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 AlaProThrLysLysSerProLeuSerGlyValSerGlnGluGlyLysGlnValGlnArg
                                                                                                                                                                                                                                                         Direct Submission
Submitted (04-DEC-1997) Molecular Biology and Oncology, UT
Southwestern Medical Conter, 6000 Harry Hines Blvd., NA8.510,
Dallas, T7.5235-9149, USA
Location/Qualifiers
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/function="BHLH transcription factor"
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Mismatches:
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.0rganism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
264. .803
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Lu, J. and Olson, E.N.
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Best Local Similarity:
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KTTLPWVPPDTKLSKLDTLRLASSYIAHLRQILANDKYENGYIHPVNLTWPFNVAGKP
ENDLKEVVTANRLCGTTAS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82 AsnAlaAlaAsnAlaArgGluArgAlaArgMetArgValLeuSerLysAlaPheSerArg 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142 AsnGlyTyrIleHisProValAsnLeuThrTrpProPheMetValAlaGlyLysProGlu 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                        mouse."
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                                                                                                                                                              male
     1. .1246
/organism="Mus musculus"
/organism="MRNA"
strain="FVB/N"
/db_xraf="taxon:10090"
/clone="MGC:58914 INAGE:6529241"
/tissue type="Colon, normal. 5 month old maily blost="Molor GAP_CO24"
/lab_host="Mulc GAP_CO24"
/note="Vector: pCMV-SPORT6"
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AF036945.1 GI:2695694
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Unpublished

Birren B. Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S. Barrata, N., Bastien, V., Bogualavkiy, L., Boukhgalter, B., Barrata, N., Campopiano, A., Chang, J., Chazaro, B., Choege, Y., Colangelo, M., Cannopiano, A., Chang, J., Gargelo, R., Cangrellano, K., Dawar, K., Diaz, J. S., Dodge, S., Faro, S., Ferreira P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Fierre, N., GitzHugh, M., Karatas, A., Hulne, M., Illev, I., Johnson, R., Jones C., Ramat, A., Karatas, A., Mcrhon, L., Hulne, M., Line, T., Johnson, R., Jones C., Ramat, A., Karatas, A., Marquis, N., Mathews, C., McCarthy, M., McEwan, P., McKernan, K., Marquis, N., Mathews, C., Northo, C., Norman, C.H., O'Connor, T., O'
                                                                                                                                                                                                                                                                                                                                                                                                                      AC101292 197332 bp DNA linear HTG 21-AUG-2002
Mus musculus clone RP23-103E4, WORKING DRAFT SEQUENCE, 27 unordered
                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 187332)
Birren, B. Nusbaum, C. and Lander, E. Mus musculus, clone RP23-10354
Unpublished
                                                                       rleuArgleuAlaSerSerTyrIleAlaHisLeuArgGlnIleLeuAlaAsnAspLysTy 140
                                                                                                                      620 ecrcadecredecrecederacaredeceaerreadecagarecrederaacaaaaaaaaa 679
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                     cagacrcaagaccaccrcaccrcagaracccccaaacaccaagcrcrccaagcraacac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACI01292.2 GI:22381296
HTG: HTGS PRASE1; HTGS DRAFT; HTGS_FULLTOP.
Mus musculus (house mouse)
Mus musculus
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                          260
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/db_xref="G1:2745887"
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ROSPOKGRGGLGKRRRAPTKKSPLSGVSQEGKQVQRNAANARERARMRVLSKAFSRL
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ESDLKEVVTASRLCGTTAS"
                                                                                               1 (bases 1 to 1254)
duagdin,5.E., Vanden Heuvel,G.B. and Igarashi,P.
Pod-1, a mesoderm-specific basic-helix-loop-helix protein expressed in mesenchymal and glomerular epithelial cells in the developing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      261 ATGTCCACCGGCTCCCTCAGCGATGTGGAGGTCTAAGAGGTGGAGATGTTGGAATGT 320
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                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                  Quaggin,S.E., Vanden Heuvel,G.B. and Igarashi,P.
Direct Submission
Submitted (24-NOV-1997) Internal Medicine, Yale University, 333
Cedar Street, New Haven, CT 06520-8029, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MetSerThrGlySerLeuSerAspValGluAspLeuGluValGluWetLeuGluCys
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product="mesoderm-specific basic-helix-loop-helix
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/gene="POD1"
/note="encodes basic-helix-loop-helix domain"
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Matches:
Conservative:
Mismatches:
Indels:
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Homo sapiens (human)
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Best Local Similarity:
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TITLE JOURNAL COMMENT

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contig of 8301 bp in length
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...23755
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/mol_type="genomic DNA"
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/clone="RP23-103E4"
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Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Valel, R., Vo.A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Direct Submission

Bubmitted (21-A07-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Aug 21, 2002 this sequence version replaced gi:17060067.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                          arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                Center clone name: 101_B 4

Center clone name: 101_B 4

Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 18339 bases at least Q40

Consensus quality: 183759 bases at least Q20

Insert size: 195000; agarose-fp

Insert size: 195000; agarose-fp

Quality coverage: 6.4 in Q20 bases; sum-of-contigs
Quality coverage: 6.8 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: This is a 'working draft' sequence. It currently consists of 27 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                    Contact: sequence submissions@genome.wi.mit.edu
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1: contig of 2185 bp in length
gap of 100 bp
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f 1166 bp in length
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24555: gap of 100
24529: contig of 2
24629: gap of 100
255795: contig of 1
25574: contig of 1
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Matches:
Conservative:
Mismatches:
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HTG; HTGS PHASE1; HTGS DRAFT; I
Rattus norvegicus (Norway rat)
Rattus norvegicus
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Submitted (20-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 20, 2002 this sequence version replaced gi:22856693.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E.,
Mawhiney, S., McLeod, M.P., McNeill, T.Z., Meenen, E.,
Milosavljevic, A., Milnar, G., Millja, B., Montemayor, J., Moore, S.,
Morgan, M., Morris, K., Morris, S., Munidaaa, M., Murphy, M., Nair, L.,
Nardelemeh, C., Okudul, G., Olarnpunsagon, A., Pal, S., Parks, K.,
Pasternak, S., Paul, H., Perez, A., Perez, L., Pramkoch, C.,
Plopper, F. Poindexter, A., Popovic, D., Primus, E., Pu, L.-L.,
Plopper, F. Poindexter, A., Popovic, D., Primus, E., Pu, L.-L.,
Reilly, B., Reilly, M., Rachin, Y., Rachter, M., Redjer, M.A., Reigh, R.,
Reilly, B., Reilly, M., Rachin, Y., Rachter, M., Robe, R., Ridges, F.,
Rives, C., Rodkey, T., Rojas, A., Rose, M., Robe, R., Riges, F.,
Randers, W., Savery, G., Scherer, S., Soct, G., Shatsman, S., Shen, H.,
Shetty, J., Shavatteborn, A., Sisson, I., Sitter, C.D., Smajs, D.,
Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J.,
Steimle, M., Strong, R., Tingey, A., Trejos, Z., Usmani, K.,
Valas, R., Verra, V., Villasana, D., Walter, M., Warker, B., Wang, J.,
Waright, R., Warren, J., Walten, R., Weoden, H., Worley, K.,
Wright, D., Waright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, L.,
Walisho, D., Waright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,
Yu, F., Zhang, J., and Gibbs, R.A.
Direct Submission
AL Unpublished
AL Unpublished
Baylor Plaza, Houston, TX 77030, USA
Baylor Plaza, Houston, TX 77030, USA
Baylor Plaza, Houston, Change Sequencing Center, Department of Molecular and Human Geneme Sequencing Center, Department of Note Sequencing Consertium.
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Baylor Plaza, Houston, TX 77030, USA
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NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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sequencing project.
This sequence is from the
BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST cDNA collection,
from a library constructed by Elizabeth Bosch. cDNA was prepared
from RNA extracted from ovary, normalised, and poly A-trimmed.
BCORI.NotI cut cDNA was then ligated into the vector. Vector:
PBluescript II KS(+); Site_I: ECORI; Site_2: NotI Host: Escherichia
coli DH10B.
On Apr 1, 2004 this sequence version replaced gi:41633328.
BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST Gallus gallus cDNA
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Gallus gallus

Gallus gallus

Gallus gallus

Bukaryota, Metacos, Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria Aves; Neognathae; Galliformes; Phasianidae;

Phasianinae; Gallus.

E 1 (Asses I to 1164)

Boardman, P.E., Bonfield, J.K., Brown, W.R.A., Carder, C., Chalk, S.E., Croning, M.D.R., Davies, R.M., Francis, M.D., Grafham, D.V., Hubbard, S.J., Humphray, S.J., Hunt, P.J., Maddison, M., McLaren, S.R., Niblett, D., Overton, I.M., Rogers, J., Scott, C.E., Taylor, R.G., Tickle, C. and Wilson, S.A.

Direct Submission

L Submitted (129-MAR-2004) Sanger Institute, Hinxton, Cambridgeshire, CEIO 1SA, UK. E-mail enquiries: chickest@bms.umist.ac.uk
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    This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                 232705: contig of 232705 bp in length 232706 232805: gap of unknown length 234024 234024 234024 234024 234123; gap of unknown length 234024 234123; gap of unknown length 234124 241544; contig of 7421 bp in length. Location/Qualifiers // organism="Rattus norvegicus" // milling // clone="CH230-58J14"
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BX932800 GI:46017571
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/note="wgs_contig"
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LeudrgGlnIleLeudladsnaspLysTyrGludsnGlyTyrIleHisProValAsnLeu 150
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1. 1164, with the state of the 
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us-09-701-674a-23.rge

Run

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CQ718038 Sequence
AF024718 Mus muscu
AF029753 Mus muscu
AF026953 Mus muscu
BC05325 Mus muscu
BC05325 Mus muscu
BC05325 Mus muscu
BX032800 Gallus ga
BC073597 Xenopus 1
AX66071 Xenopus 1
AX66071 Xenopus 1
AX66071 Xenopus 1
AL356109 Human DNA
AC101292 Mus muscu
AC101292 Mus muscu
AC101292 Mus muscu
AC115183 Rattus no
BC0673516 Danio rer
BC0067313 Homo sapi
BC067827 Homo sapi
BC067827 Homo sapi
BC067827 Homo sapi
BC067827 Homo sapi
AC104012 Homo sapi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Germany
KZPD; RZPDc834B111D, ORFNO 76
www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPDc834B111D RZPDLIB;
Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD LIB No.
834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (Dases 1 to 537)

Ebert, L., Schick, M., Neubert, P., Schatten, R., Henze, S. and Korn, B. Cloning of human full open reading frames in Gateway (TM) system entry vector (pDONR201)

Unpublished

2 (Dases 1 to 537)

2 (Dases 1 to 537)

Ebert, L., Schick, M., Neubert, P., Schatten, R., Henze, S. and Korn, B. Direct Submission

Submitted (18-MAY-2004) RZPD Deutsches Ressourcenzentrum fuer
AF047419 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CR450293.1 GI:47496532
Full ORF shuttle clone, Gateway(TM), complete cds.
Homo sapiens (human)
Homo sapiens
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9 AZ101282

2 AC115183

10 AF061752

2 CR230074

2 CR230565

2 CR230565

2 CR230565

2 CR230565

2 CR230565

3 CR230565

4 CR230565

6 CQ717187

6 CQ717187

6 AX281674

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10 AF080216

10 AF08026

2 AC022867

10 AC022867

11 AC112876

10 AC13255

2 AC112783

2 AC112783

3 AC13255

6 AX333347

6 AX333347

6 AX333347

8 AC14743

3 DMA/729
                                   AF047418
AF029753
AB009453
AF035717
BC053525
AF036945
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VERSION
KEYWORDS
SOURCE
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CR450293
LOCUS
DEFINITION
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AUTHORS
TITLE
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AUTHORS
TITLE
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      0 0 0 0 0
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-MODEL=frame+_D2n.model -DEV=xlh
-MODEL=frame+_D2n.model -DEV=xlh
-Q=/Cq21_21/USPTO spool_h/USO9701674/runat_15122004_100440_27505/app_query.fasta_1.327
-Q=/Cq21_21/USPTO spool_h/USO9701674/runat_15122004_100440_27505/app_query.fasta_1.327
-DEVENTION=200 -TFNE_SCORE=pct -THN_RINAL=00-1.-LOOPGL=0.LOOPERT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITS=bits -START=1 -END=-1 -MATRIX=DO -THR_NIN=0 -ALIGN=15 -MODE=LOCAL
-UNITSH=pto -NORM=ext -HEAPE1ZE=500 -MINISH=0 -ALIGN=15 -MODE=LOCAL
-USER=USO9701674_@CGN 1 1 3731_@runat_15122004_100440_27505 -NCFU=6 -ICFU=3
-NO_MARP -LARREQUERY -NGG_SCORES=0 -MATRI -DEPREDCK=100 -LONGLOG
-DSW_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CR450293 Homo sapi
BD211771 Proteins
BC025697 Homo sapi
AF035718 Homo sapi
                                                                                                                                     December 16, 2004, 20:19:00 ; Search time 3794 Seconds (without alignments) 2231.117 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                                                                                                                                    US-09-701-674A-23
917
1 MSTGSLSDVEDLQEVEMLEC......PESDLKEVVTASRLCGTTAS
                        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                   nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                     4526729 seqs, 23644849745 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                             of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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BD211771
BC025697
AF035718
                                                                                                                                                                                                                                                                                                                   Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seg length: 2000000000
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EUKARYOCTA METAZOA; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(CE 10, (Daeca 1 to 1272)

(CE 11, P., Yue, H., Tang, Y.T., Hillman, J.L., Bandman, O., Corley, N.C., Guegler, K.J., Gorgone, G.A., Baughn, M.R., Patterson, C. and Lu, D.A.M.

Proteins regulating gene expression

Patent: JP 2002517246-A 23 18-JUN-2002;

INCYTE PHARMACEUTICALS INC

OS Homo sapiens (human)

PN JP 2002517246-A/23

PD 18-JUN-2002

PP 11-JUN-1998 US 60/00553586

PR 12-JUN-1998 US 60/104624

PR 13-JUN-1998 US 60/104624

PR 13-JUN-1998 US 60/104624

PR 14-OCT-1998 US 60/104624

PR 14-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAT 17-JUL-2003
                 361 CTCAGGCTGGCGTCCAGCTACATCGCCCACTTGAGGCAGATCCTGGCTAACGACAAATAC 420
                                                                                                                                                                                                                                     141 GluAsnGlyTyrIleHisProValAsnLeuThrTrpProPheMetValAlaGlyLysPro 160
                                                                                                                              LeuArgLeuAlaSerSerTyrlleAlaHisLeuArgGlnIleLeuAlaAsnAspLysTyr 140
                                                                                                                                                                                                                                                                                           421 GAGAACGGGTACATTCACCCGGTCAACCTGACGTGGCCCTTTATGGTGGCCGGGAAACCC 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 268 ATGTCCACCGGCTCCCTCAGCGATGTGGAGGACCTTCAAGAGGTGGAGATGTTGGAATGT 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 AspGlyLeuLysMetAspSerAsnLysGluPheValThrSerAsnGluSerThrGluGlu 40
                                                                                                                                                                                                                                                                                                                                                1 MetSerThrGlySerLeuSerAspValGluAspLeuGlnGluValGluMetLeuGluCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism='Homo sapiens (human)'.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Pred. No.:
                                                                                                                           121
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VERSION
KEYWORDS
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AUTHORS
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JOURNAL
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BD211771
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                                                                                                                                                                                                                          This clone is available from RZDD, context RZDD (customer.servicedrzdd.de) for further information. This CLOs clone is a part of a collection of human full length expression clones generated by RZDD.

This CDS has been cloned without stopcodon.

The CDS has been inserted into pDONR201 via a BP Clonase(TM) reaction. Additional sequence has been added in front of the start codon (ATG); att. .AAAAA GCT GCC ACC CCT GGT CCA GGT (ATG) After the last codon additional sequence has been added: CCA GCC CCA GCG Gin front of the 3' att site (AC CCA GGT TTC TT). Compared to the reference sequence NM_003206 we did not find any amino acid exchanges; clone distribution: http://www.rzpd.de/products/orfclones/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
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KTTLBWVPPDTKLSKLDTLRLASSYIAHLRQILANDKYENGYIHPVNLTWPFMVAGKP
ESDLKEVVTASRLCGTTAS"
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www.rzpd.de/cgi-bin/products/showLib.pl.cgi/response?libNo=834
www.rzpd.de/products/orfclones/
Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH,
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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Indels:
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VIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Parayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing center (NISC)
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc mgc@nhgri.nih.gov/
Contact: nisc mgc@nhgri.nih.gov/
Contact: nisc mgc@nhgri.nih.gov/
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin.B.,
Blakesley,R.W., Boulfard,G.G., Breon,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi.P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
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TBurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MSTGSLSDVEDLQEVEMLECDGLKMDSNKEFVTSNESTEESSNC
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ESDLKEVVTASRLGGTTAS"
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4507394.
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/tissue type="Pancreas, Spleen, adult pooled"

/clone_lib="NIH_MGC_120"

/clone_lib="NIH_MGC_120"

/note="Vector: pCMV-SPORT6"
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|db_xref="G1:19344016"
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|db_xref="MIM:603306"
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2607. 799
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Submitted (06-MAR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
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Homo sapiens transcription factor 21, transcript variant 1, mRNA (CDNA clone MGC:34534 IMAGE:5221575), complete cds.

BC025697
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                                                                                                                                                                 ArgAsnAlaAsnAlaArgGluArgAlaArgMetArgValLeuSerLysAlaPheSer
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                                                                                                                                                                                                                                                      CECAACECCECCAACECECEAGAGECEGECCCECATECEAGTECTGAGECAAGGCCTTCTCC
             human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Homo sapiens
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2 (bases 1 to 1257)
Robb, L. and Mifsud, L.
Direct Submission
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Best Local Similarity:
                                                                Scores:
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Homo sapiens mesoderm-specific basic-helix-loop-helix protein
(PDD1) mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quaggin, S.E., Vanden Heuvel, G.B. and Igarashi, P.
Pod-1, a mesoderm-specific basic-helix-loop-helix protein expressed
in mesenchymal and glomerular epithelial cells in the developing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fprotein_id="AAC62514.1"
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ESDLKEVVTASRLCGTTAS"
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                                                              AAGGCCCCACCAAGAAGAAGACCCCCTGAGCGGGGTAAGCAGGAGGAAGGTCAG 499
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 1254)

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Quaggin, S.E., Vanden Heuvel, G.B. and Igarashi, P.
Direct Submission
Submitted (24-NOV-1997) Internal Medicine, Yale University, 333
Cedar Street, New Haven, CT 06520-8029, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                    GluSerAspLeuLysGluValValThrAlaSerArgLeuCysGlyThrThrAlaSer 179
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                                                                                                        81 ArgAsnAlaAlaAsnAlaArgGluArgAlaArgMetArgValLeuSerLysAlaPheSer
                                                                                                                         CGCAACGCCGCCAACGCGCGAGAGCGGGCCCGCATGCGAGTGCTGAGCAAGCCTTCTCCC
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                                                                                                                                                                                                                                                                                  141 GluAsnGlyTyrIleHisProValAsnLeuThrTrpProPheMetValAlaGlyLysPro
                 LysAlaProThrLysLysSerProLeuSerGlyValSerGlnGluGlyLysGlnValGln
/note="Pod-1"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="6"
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Mech. Dev. 71 (1-2), 37-48 (1998)
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/gene="POD1"
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Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1257)
Robb,L., Mifeud,L., Hartley,L., Biben,C., Copeland,N.G.,
6311bert,D.J., Jenkins,N.A. and Harvey,R.P.
epicardin: A novel basic helix-loop-helix transcription factor gene expressed in epicardium, branchial arch mybblasts, and mesenchyme of developing lung, gut, kidney, and gonads

Dev. Dyn. 213 (1), 105-113 (1998)

SUBLE CONTROL OF THE CONT
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/gene="POD1"
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Homo sapiens epicardin mRNA, complete cds.
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US-09-701-674A-23 (1-179) x CQ718038
             GI:42278895
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904.00
99.44%
99.44%
98.58%
                                    Homo sapiens
Homo sapiens
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Best Local Similarity:
Query Match:
DB:
  CQ718038
CQ718038.1
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ESDLKEVVTASRLCGTTAS"
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  Eliza
                                                                                                          /function="basic helix-loop-helix transcription factor"
/note="expressed in embryonic epicardium and
mesenchyme-derived tissues of lung, gut, kidney, and
  and Cancer, Walter and Eliza
PO Royal Melbourne Hospital,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GluSerAspLeuLysGluValValThrAlaSerArgLeuCysGlyThrThrAlaSer 179
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Conservative:
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Submitted (10-FEB-1998) Haematology an Hall Institute of Medical Research, PO Melbourne, VIC 3050, Australia Location/Qualifiers 1.1257 /organism="Homo sapiens" /mol_type="mRNA" /db xref="taxon:9606" 260-799
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Homo sajiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       504 CGCAACGCCGCCAACGCGCGAGAGCGGGCCCGCATGCGAGTGCTGAGCAAGGCCTTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 LysAlaProThrLysLysSerProLeuSerGlyValSerGlnGluGlyLysGlnValGln
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                                                                                         y of
other
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Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
Kits, such as nucleic acid arrays, comprising a majority
humanexons or transcripts, for detecting expression and c
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                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                          Patent: WO 02068579-A 3972 06-SEP-2002;
PE Corporation (NY) (US)
Location/Qualifiers
1. 1259
/ organism="Homo sapiens"
/ nol type="unassigned DNA"
/db_xref="taxon:9606"
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ROSPOKGRGGGGRRRKAPPKKSPLSGVSOGGKQVQRNAANARERARKVLSKAFSRL
KTTLDWVPPDTKLSKLDTLALASSYIAHLRQILANDKYENGYIHPVNLTWPFWVAGKP
ENDLKEVVTPNRLGGTTAS"
                                                                                                                                                                                                                                                                                                                      AF029753 1 1217 bp mRNA linear ROD 25-FEB-2000 Was musculus basic helix-loop-helix factor Corl mRNA, complete cds. AF029753.1 GI:2613018
                                          121 LeuArgleuAlaSerSerTyrIleAlaHisLeuArgGlnIleLeuAlaAsnAspLysTyr 140
                                                                       559 CTCAGGCTGGCGTCCAGCTACATCGCTCACTTAAGGCAGATCCTGGCCAACGACAAGTAC 618
                                                                                                                      141 GluAsnGlyTyrIleHisProValAsnLeuThrTrpProPheMetValAlaGlyLysPro 160
      199 AGGCTCAAGACCACCCTGCCCTGGGTGCCCCCGGACACCCAAGCTCTCCAAGCTGGACACT 558
                                                                                                                                             619 GAGAACGGTTACATCACCCAGTCAACCTGACGTGGCCCTTTATGGTGGCGCGCAAACCA 678
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Hidai, H., Bardales, R., Goodwin, R., Quertermous, T. and Quertermous, E.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cloning of capsulin, a basic helix-loop-helix factor expressed in progenitor cells of the pericardium and the coronary arteries Mech. Dev. 73 (1), 33-43 (1998) 1026
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2 (bases 1 to 1217)
Quertermous, T., Quertermous, B.E., Hidai, H., Fadel, B., Boutet, S.C. and Bardales, R.
                                                                                                                                                                                                                         679 GAGAATGACCTGAAGGAAAGGAGTGACCGCCAACCGCTTGTGTGGGAACTACAGCATCC 735
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (10-OCT-1997) Department of Medicine, Division of Cardiology, Stanford University, Falk Bldg, 300 Pasteur Drive, Stanford, CA, 94:305, USA, Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .1217. xcorinters
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/db_xref="texon:10090"
/tisue_type="pericardium and coronary arteries"
1. .1217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
/product="haals helix-loop-helix factor Corl"
/protoin id="haals4256.1"
/db_xref="G1:2613019"
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Conservative:
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/gene="Cor1"
/function="transcription factor"
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Mus musculus
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Pred. No.:
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            Mus musculus (house mouse)

Mus musculus

Bukaryota, Metazoa: Chordata, Craniata, Vertebrata, Buteleostomi,

Bukaryota, Metazoa: Chordata, Sciurognathi, Muridae, Murinae, Mus.

1 (bases 1 to 1202)

1 (bases 1 to 1202)

Robb.L., Mifsud,L., Hartley,L., Biben,C., Copeland,N.G.,

Gilbert,D.J., Jenkins,N.A. and Harvey,R.P.

Gilbert,D.J., Jenkins, N.A. and Harvey,R.P.

expressed in epicardium, branchial arch myoblasts, and mesenchyme of developing lung, gut, kidney, and gonads

Dev. Dyn. 213 (1), 105-113 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="WSTGSLSDVEDLQEVEMLDCDSLKVDSNKEFGTSNESTEEGSNC
ENGSPQKGRGGLGKRRKAPTKKSPLSGYSQEGKQVQRNAANARERARNGVLSKAFSRL
KTTLPWVPPDTKLSKLDTLRLASSYIAHLRQILANDKYENGYIHPVNLTWPFMVAGKP
ENDLKEVVTANRLCGTTAS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /function="basic helix-loop-helix transcription factor"
//function="basic helix-loop-helix transcription factor"
//note="expressed in embryonic epicardium and
mesenchyme-derived tissues of lung, gut, kidney, and
gonad"
                                                                                                                                                                                                                                                                                                                                         and Cancer, Walter and Eliza
PO Royal Melbourne Hospital,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  199 ATGTCCACTGGCTCCCTCAGCGATGTAGAAGACCTTCAAGAGGTGGAGGTGCTGGACTGT
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Robb,L. and Mifsud,L.
Direct Submission
Submitted (10-FEB-1998) Haematology an Hall Institute of Medical Research, PO Melbourne, VIC 3050, Australia
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199. .738
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AF035717 1240 bp mRNA linear ROD 05-OCT-1998 Mus musculus mesoderm-specific basic-helix-loop-helix protein (Podl) mRNA, complete cds.
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Quaggin, S.B., Vanden Heuvel, G.B. and Igarashi, P.
Pod-1, a mesoderm-specific basic-helix-loop-helix protein expressed in mesenchymal and glomerular epithelial cells in the developing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       583 CTCAGGCTGCCGTCCAGCTACATCGCTCACTTAAGGCAGATCCTGGCCAAACGACAAGTAC 642
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      463 cecaacecedeccaarecreereaceeecceeareceegreereaceaaeecrrerec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 | 111111 | 111111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 
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                                                                                                       Length:
Matches:
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Mismatches:
Indels:
Gaps:
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Mech. Dev. 71 (1-2), 37-48 (1998)
98175875
  /note="17 A nucleotides"
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                                                                                                       2.89e-73
887.00
98.32%
96.09%
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Best Local Similarity:
Query Match:
DB:
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/ organism="mRNA"

/ db_xref="raxon:10090"

223. 762

/ function="transcription factor"

/ note="basic helix-loop-helix gene"

/ codon:start=1

/ codon:start=1

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/ protein_id="BAA23883.1"

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/ translation="NSTGSLSDVEDIGEVEMIDCDSIKVDSNKEFGTSNESTEEGSNC

ENGSPOKGRGGIGKRRKAPTKKSPLSGVSQEGKQVQRNAANARERARMRVLSKAFSRL

KTTLPWVPPDTKLSKLDTLRASSYIAHIRQILANDKYENGYIHPVNLTWPFWVAGKF

ENDLEVVTANRLCGTTAS"
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                                                                                  ArgleulysThrLeuProTrpValProProAspThrLysLeuSerLysLeuAspThr 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTCAGGCTGGCGTCCAGCTACATCGCTCACTTAAGGCAGATCCTGGCCAACGACAAGTAC 632
213 ATGTCCACTGGCTCCCTCAGCGATGTAGAAGACCTTCAAGAGGTGGAGATGCTGGACTGT 272
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ABOUNDS.1. GHIZBYBELL/
AND MASSALL GHIZBYBELL/
MAS MUSCULUS

Nus musculus

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

E 1 (bases 1 to 1220)

I Tamura, and Nakatsuji, N.

I Published Only in DataBase (1997)

E 2 (bases 1 to 1220)

E 2 (bases 1 to 1220)

I Tamura, M. and Nakatsuji, N.

Direct Submission

L Submitted (04-DEC-1997) Masaru Tamura, National Institute of Genetics; Mammalian Development; Yata 1111, Mishima, Shizuoka 411, Japan (E-mail:matamura@lab.nig.ac.jp, Tel:+81-559-81-6832,
                                                                                                                                                                  9
                                                                                                                                                                                                                                                                            LysAlaProThrLysLysSerProLeuSerGlyValSerGlnGluGlyLysGlnValGln 80
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Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                    333 GGCTCCAACTGCGAGAACGGGTCTCCACAGAAGGGTCGCGGTGGCCTAGGCAAGAGGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       633 GAGAACGGTTACATTCACTCAGTCAACCTGACGTGGCCCTTTATGGTGGCCCGCAAACCA
                                                        AspGlyLeuLysMetAspSerAsnLysGluPheValThrSerAsnGluSerThrGluGlu
                                                                                                                                                                  41 SerSerAsnCysGluAsnGlySerProGlnLysGlyArgGlyGlyLeuGlyLysArgArg
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Mus musculus mRNA for nephgonadin,
AB009453
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Location/Qualifiers
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AB009453
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120

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100 522

282

1220 172 4 3 0

342

40

402 9

80

140

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VIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-ramail.nih.gov
Tissue Procurement: Jeffrey B. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Maryland;
Web Site: http://www.nisc.nih.gov/
Gaithersburg, Maryland;
Web Site: http://www.nisc.nih.gov/
Contact: nisc.mgc@nhgri.nih.gov/
Contact: nisc.mgc@nhgri.nih.gov/
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Hadpidhi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                              Mus musculus (house mouse)

Mus musculus (house mouse)

Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Musmalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

I (bases 1 to 1246)

Straubberg, E., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.P., Jordan, H., More, T., Rang, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marushina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.B., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Rand, S.S., Loquellano, N.A., Peters, G.J.,

Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Rahey, V., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Rodrigues, S.,

Butterfield, Y.S., Krzywinski, M.I., Sakhutz, J., Shevchenko, Y.,

Butterfield, Y.S., Krzywinski, M.I., Sakhitz, J., Smailus, D.E.,

Schnerch, A., Schein, J.E., Ores, S.J. and Mazra, M.A.,

Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 108 Rvw: p Column: 16.
Location/Qualifiers
                                                        BC053525 1246 bp mRNA linear ROD 30-JUN-2004
Mus musculus transcription factor 21, mRNA (cDNA clone MGC:58914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (09-UN-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
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/strain="PVB\N"
/db xrefe="taxon:10090"
/clone="MGC:58914 IMAGE:6529241"
/tissue_type="Colon, normal. 5 month old male mouse."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                IMAGE: 6529241), complete cds.
                                                                                                                                                                     BC053525.1 GI:31566109
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Strausberg, R.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              160
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                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
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Cedar Street, New Haven, CT 06520-8029, USA Location/Qualifiers
1. .1240
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENDLKEVVTANRLCGTTAS"
                                                                                                                                                                                                                                                                      226 .765
/gene="Pod1"
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                                                                                                                                                                                                                                                    gene="Pod1"
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887.00
98.32$
96.09$
96.73$
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ENDLKEVVTANRLCGTTAS"
                                                                                                                                                            Lu,J., Richardson,J.A. and Olson,E.N. Capsulin: a novel bHLH transcription factor expressed in epicardial progenitors and mesenchyme of visceral organs Mech. Dev. 73 (1), 23-32 (1998)
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Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B84 GGCTCCAACTGCGAGAACGGGTCTCCACAGAAGGGTCGCGCTGGCCTAGGCAAGAGGAGGT
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                                                                                                                                                                                                                                                                                                    Lu.7. and Olson, E.N.
Direct Submission
Submitted (04-DEC-1997) Molecular Biology and Oncology, UT
Southwestern Medical Center, 6000 Harry Hines Blvd., NA8.510,
Dallas, T7.5225-9148, USA
Location/Qualifiers
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172
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/function="BHLH transcription factor"
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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264. 803
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                                                                                         Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Rodentia,
1 (bases 1 to 1267)
                                          Mus musculus (house mouse)
Mus musculus
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GI:2695694
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VERSION
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ENDLKEVVTANRLCGTTAS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          353 GGCTCCAACTGCGAGAACGGGTCTCCACAGAAGGGTCGCGGTGGCCTAGGCAAGAGGAGG
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                                                                                    /gene="Tof21"
/note="synonyms: epc, Pod1, capsulin, epicardin, Pod db_xref="LocusID:21412"
/db_xref="MG1:1202715"
233. .772
/gene="Tof21"
/gene="Tof21"
/product="transcription factor 21"
/protein id="AAH55525.1"
/db_xref="[a:13566110"
/db_xref="LocusID:21412"
/db_xref="MG1:1202715"
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Mus musculus capsulin mRNA, complete cds
AF036945
                                               note="Vector: pCMV-SPORT6"
clone lib="NCI CGAP_Co24"
lab host="DH10B"
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Strausberg, L. (Dases 1 to 965)

Strausberg, L. (Feingold, E.A., Grouse, L.H., Derge, J.G., Strausberg, R.L., Feingold, E.A., Wagner, L., Shemmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Stapleton, M., Shange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., Mare, M. (Gay, L.J., Hulyk, S.W., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Worley, K.C., Hale, S., Garcia, A.M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchen, E.D., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Schmutz, J., Myers, R., Schein, J. B., Nords, M., Schein, J. B., Nords, M., Schein, J. B., Nords, M., Sanilus, D.E., Schnerch, A., Schein, J. B., Nords, M., Sanilus, D.E., Hength H., Marner, M. M., Schein, J. B., Marner, M. M., Schein, J. B., Marner, M. M., Schmutz, J., Myers, M. M., Schein, J. B., Marner, M., A., Schein, J. B., Marner, M., A., Schein, J. B., Marner, M., A., Marner, M., M., Schein, J. B., Marner, M., Schein, J. J., Schein, J. J., Schein, J. J., Schein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Senoyss laevis transcription factor 21, mRNA (cDNA clone MGC:82899) MAGE:5212805), complete cds.
                                                                                                                                                                                                               140
                                                                                                                                                                                                                                                                                                                                                                                                                        GluAsnGlyTyrIleHisProValAsnLeuThrTrpProPheMetValAlaGlyLysPro 160
                                                   406
                                                                                                                                                            466
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                                                                                                                                                                                                                                                                                                                                                                        527 TIGAGGCIGGCCICCAGCIACAICGCACACCIGAGGAAAICCIGGCCAACGACAAGIAC 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Klein, S. L., Strausberg, R. L., Wagner, L., Pontius, J., Clifton, S.W. and Richardson, P.
                               161 GluSerAspLeuLysGluValValThrAlaSerArgLeuCysGlyThrThrAlaSer 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                           81 ArgAsnAlaAsnAlaArgGluArgAlaArgMetArgValLeuSerLysAlaPheSer
                                                                                                                                             AGABACGCTGCCAACGCAAGGGAGAGGCAAGGATGAGGTCCTTAGCAAAGCCTTCTCC
LysAlaProThrLysLysSerProLeuSerGlyValSerGlnGluGlyLysGlnValGln
                                                                                                                                                                                                                                                                                                                        LeuArgLeuAlaSerSerTyrlleAlaHisLeuArgGlnIleLeuAlaAsnAspLysTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleost
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopus laevis (African clawed frog)
Xenopus laevis
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BC073597.1 GI:49256164
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Klein, S. and Gerhar
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TITLE
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This sequence is from the BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST cDNA collection, from a library constructed by Elizabeth Bosch. cDNA was prepared from RNA extracted from ovary, normalised, and poly A-trimmed. EcoR1-NotI cut cDNA was then ligated into the vector. Vector: pBluescript II KS(+); Site_1: EcoRI; Site_2: NotI Host: Escherichia coli DH10B.
                                                                                                                                                                                                                                                                                                 VRT 30-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

1 (bases 1 to 1164)

Boardman, P. E., Bonfield, J. K., Brown, W.R.A., Carder, C., Chalk, S.E., Croning, M.D.R., Davies, R.M., Francis, M.D., Grafham, D.V., Humbard, S.J., Hunt, P.J., Maddison, M., Mclaren, S.R., Niblett, D., Overtron, I. M., Rogers, J., Scott, C.E., Taylor, R.G., Takle, C. and Wilson, S.A.
                            | GluAsnGlyTyr1|eHisProValAsnLeuThrTrpProPheMetValAlaGlyLysPro 160
                                                           684 GAGAACGGTTACATTCACCCCAGTCAACCTGGCCCTTTATGGTGGCCGGCAAACCA 743
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (29-MAR-2004) Sanger Institute, Hinxton, Cambridgeshire, Calb 15A, UK. E-mail enquiries: chickestdebms.umistr.ac.ud
On Apr 1, 2004 this sequence version replaced gi:41633328.
BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST Gallus gallus cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20
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                                                                                                                                     GluSerAspleuLysGluValValThrAlaSerArgleuCysGlyThrThrAlaSer 179
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Gallus gallus finished cDNA, clone ChEST265h24.
BX932800
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Gallus gallus (chicken)
Gallus gallus
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Query Match:
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ENDLKEVVSTSRLGGPTAS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VRT 20-JUL-2004
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                                                                                                                                                                  101 ArgleulysThrThrLeuProTrpValProProAspThrLysLeuSerLysLeuAspThr 120
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                                                                                                          264 AGGAATGCAGCCAATGCCAGGGAGAGAGCCAGGATGAGGGTGCTAAGCAAAGCAAAGCTTTTCT 323
                                                                                                                                                                                                                                                       LeuArgleuAlaSerSerTyrIleAlaHisLeuArgGlnIleLeuAlaAsnAspLysTyr 140
                                                                                                                                                                                                                                                                                                                                       141 GluasnGlyTyrIleHisProValAsnLeuThrTrpProPheMetValAlaGlyLysPro 160
                                                                                                                                                                                                                                                                                                                                                             444 GAAAATGGCTACATCCATCAGTTAACCTGACTTGGCCCTTTATGGTGGCTGGAAAACCA 503
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="basic helix-loop-helix transcription factor;
capsulin; epicardin; podocyte-expressed 1; Podl; Pod-1"
                                                                                                                                                                                                                                                                                                                                                                                                                          161 GluSerAspLeuLysGluValValThrAlaSerArgLeuCysGlyThrThrAlaSer 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                  324 AGGCTAAAAGACCACTTTGCCTTGGGTGCCTCCAGACACCAAACTTTCCAAGCTGGACACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xenopodinae; Xenopus; Xenopus.
1 (bases 1 to 1059)
Eid,S.r. and Brandli,A.W.
Essential function of the basic helix-loop-helix transcription factor Tcf21 (capsulin/epicardin/Pod1) for Xenopus pronephric
                            LysAlaProThrLysLysSerProLeuSerGlyValSerGlnGluGlyLysGlnValGln
                                                                                    ArgAsnAlaAlaArgGluArgAlaArgMetArgValLeuSerLysAlaPheSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AY660B71 1059 bp mRNA linear V
Xenopus laevis transcription factor 21 (Tcf21) mRNA,
AY660B71
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Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Xenopus laevis"
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1. .1059
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                                                                                                                                                                                  Linguage Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Featherstone, Malachi Griffith, Obl Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Perrescu, Anna Liisa Prahbu, Barvaneh Saeedi, J. W. Santos, Angelique Schnerch, Ursula Skalska, Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie Schein, Asim Siddiqui, Rob Holt, Marco Marra.
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ENDLKEVVSTSRLGGPTAS"
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NIH-MGC Project
Contact: XGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Igor Dawid
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
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info@bcgsc.bc.ca
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	7ys 20      GT 193	31u 40     3AG 253	Arg 60     AGA 313	31n 80    2AG 373	Ser 100       CT 433	Thr 120	Yr 140	oro 160 	179 670	
	GluMetLeuGlu(             GAAATGTTGGAA	GluSerThrGlu( :::    GACAGCAATGAG	LeuGlyLysArgi          CGGGCAAGAGG	31yLysglnval(             3gCAAGCAGGTC	SerLysAlaPhe(            AGCAAAGCCTTT	Serbysteuasp               CCAAGCTGGAC	AlaAsnAspLys? 	ValalaglyLysi            5TGGCTGGAAAA	ThrThrAlaser           cccacGGCATCT	
1059 1154 112 0	SlnGluVal    ::::: CAAGACATG	ThrserAsn        \TATCCAAC	ArgGlyGly;        AgaGGGACT	SerGinglu( :::      AaccaGGAG	Argvalleu          AGGGTGCTA	Thriysteu          accaaactt	31niletew             AAATTCTA	ProPheMet'	leuCysGly'           rGrGrGGr	
Length: Matches: Conservative Mismatches: Indels: Gaps: 1 (1-1059)	MetSerThrGlySerLeuSerAspValGluAspLeuGlnGluValGluMetLeuGluCys 	AspGlyLeuLysMetAspSerAsnLysGluPheValThrSerAsnGluSerThrGluGlu 	SerSerabnCysGluasnGlySerProGlnLysGlyArgGlyGlyLeuGlyLysArgArgArg 	LysalaproThrLysLysSerProLeuSerGlyValSerGlnGluGlyLysGlnValGln 	ArgasnalaalaasnalaargGluargalaargMetargvalbeuseriysalaPheser 	ArgleulysThrThrLeuProTrpValProProAspThrLysLeuSerLysLeuAspThr 	Leuargleualasersertyrilealahisleuargginileleualaasnasplysfyr 	GluasnGlyTyrIleHisProValAsnLeuThrTrpProPheMetValalaGlyLysPro 	GluserAspLeulysGluValValValThrAlaserArgLeuCysGlyThrThrAlaser     :::	, 23:15:58
1.32e-65 804.00 : 92.74% ity: 86.03% 87.68% 5 (1-179) x AY660871	arGlyserLeuser 	euLysMetAspSer ::   :::    rcaaacrggarccr	snCysGluAsnGly     :::       ccTGCGACAACGGT	roThrLysLysSer  :::          CAGCAAGAAAGT	laAlaAsnAlaArg 	/sThrThrLeuPro                     AGACCACTTTGCCT	eualaSerSerTyr 	lyTyrIleHisPro                   GCTACATCCATCCA	spieulysgluval             accrcaaggaagrg	December 16, 2004,
Scores: imilarity l Similar ch: -674A-23	1 MetserT          134 ATGTCCAC	21 AspGlyLe       : 194 GATGGCA1	41 SerSerAs         254 AGTTCAAG	61 LysalaP1        314 AAAGCCTC	81 ArgAsnA]           374 AGGAATGO	101 Argleuly          434 AGGCTAA	121 LeuArgLe           494 CTGCGGCJ	141 GluAsnG]           554 GAAAATGC	161 GluSerAe    :::   614 GAAAACGA	completed: ne : 3803 se
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                                                 OM nucleic - nucleic search, using sw model
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1. geneseqn1980s:*
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7: geneseqn2003as:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES		ID	AAZ57861	ABL65519	ABL65935	ABK64784	ABQ55427	ABL66121	ABL65571	ABK64115	ACH23969	ACH21857	AAC08260	ADK61063	ADM32307	ACA56430	AD156226	ADE25693	AAA72428	ADJ56314	AAZ50465	AAS94828	AAZ50464
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	% Ouery		100.0	45.7	45.7	45.7	41.3	36.7	36.7	36.7	34.1	23.4	19.4	18.6	18.6	16.7	16.7	16.6	16.6	16.6	16.5	16.4	14.9
		Score	1272	581	581	581	525.6	466.2	466.2	466.2	434.2	297.2	246.8	236.2	236.2	213	213	211.6	211.6	211.6	210	208.6	189.6
	Result	No.	П	7	m	4	ഗ	o o	C 7	ω U	σ	10	11	c 12	c 13	14	15	16	17	18	19	20	21

Aat21519 Human gen	Abz18589 Group III	Aad51583 Human str	Ada71938 Rice gene	Adc32623 Human nov	Adc30883 Human nov	Adq25304 Human sof	Acc62520 Human sec	Acc62491 Human sec	Abl16071 Drosophil	Abk71581 Human dit	Abg88217 Human ost		Abl08722 Drosophil	Aas76438 DNA encod	Ach89545 Human gen			Adg22344 Human sof	Abt06509 TWIST gen	Adm83716 Human twi	Adq17684 Human sof	Adq21461 Human sof	Aaf27265 Mouse ato
AAT21519	ABZ18589	AAD51583	ADA71938	ADC32623	ADC30883	ADQ25304	-	ACC62491	ABL16071	ABK71581	ABQ88217	ABL08723	ABL08722	AAS76438			ADP65052	ADQ22344	ABT06509	ADM83716	ADQ17684	ADQ21461	AAF27265
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9.3	9.9	9.9	9.9	6.5	6.5	6.5	6.5	6.5	6.5	6.4	6.2	6.1	6.1	6.1	9.9	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6
118	83.4	83.4	83.4	82.6	82.6	82.6	82.6	82.6	82.2	81.8	78.4	77.6	77.6	77.4	71.8	71.8	71.8	71.8	71.8	71.8	71.8	71.6	7.1
22	23	24	25	26	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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## ALIGNMENTS

AAZ57861 standard; cDNA; 1272 BP.

AAZ57861;

RESULT 1
AAZ57861
ID AAZ5
XX
AC AAZ5
XX

E X	11-APR-2000 (first entry)
X	Protein regulating gene expression PRGE-23 cDNA clone 3340296.
252	Protein regulating gene expression; PRGE-23; human; cancer; inflammation; anticancer; antitumour; antiinflammatory; Myc; HIH protein; gene therapy;
XX	diagnosts; ss. Homo sablens.
XELE	
XX	
X 2 :	16-DEC-1999.
Y E	11-JUN-1999; 99WO-US013281.
A	12-JUN-1998; 98US-0089629P. 29-JUL-1998; 98US-0094575P. 14-OCT-1998; 98US-0104624P.
X Z	(INCY-) INCYTE PHARM INC.
PI	Lal P, Yue H, Tang YT, Hillman JL, Bandman O, Corley NC; Guegler KJ, Gorgone GA, Baughn MR, Patterson C, Lu DAM;
X K K i	WPI; 2000-116543/10. P-PSDB; AAY58630.
XFE	New human polypeptides that regulate gene expression, for treatment, prevention and diagnosis of, e.g. cancer.
Y S	Claim 9; Page 139; 150pp; English.
<b>\$</b> 8	The present sequence is that of Incyte clone 3340296 encoding new human

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       841 CCGGGGGGAGCGGGCCCCCGGGAAGGCGACCCCTGCCTCAGTGCTCTCTGTTTCTTGCTTC
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                                                                                                                             CCGGGGGGGCCCCCGGGGAAGGCGACCCCTGCCCTCAGTGCTCTCTGTCTCTGCTTC
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protein regulating gene expression PRGE-23 (see AAYS8630). The CDNA was initially isolated from spleen tissue CDNA library SPLNOT10, and the full-length sequence assembled from overlapping clones from a number of libraries. PRGE-23 is expressed in reproductive, developmental and urologic tissues associated with cancer, inflammation and foetal protein. The invention provides PRGE polypeptides (see AAYS8608-38) protein. The invention provides PRGE polypeptides (see AAYS8608-38) and polynucleotides (see AAZ57839-68), expression exclose, agonists and antagonists. It also provides methods for diagnosing, treating or preventing disorders associated with expression of PRGE. Polynucleotides are also used as sources of probes and primers for diagnosis and monitoring of disease, also for detecting related sequences and in gene mapping
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100.0%; Score 1272; DB 3; Length 1272;
Best Local Similarity 100.0%; Pred. No. 5.1e-284;
Matches 1272; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1272 BP; 311 A; 358 C; 318 G; 285 T; 0 U; 0 Other;
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                                                                               121 GGAAACCCGAGAGTGACCTGAAAGAAGTGGTGACCGCGAGCCGCTTATGTGGAACCACCG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid; stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous; cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                                                                                                                                                                 CGTCCTGACCTTGGAGGTGCGAGTCTGGGAAAGGCGCGCTCCCGGGGGGANGCGCNCNCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCTCTGTCCCCACCCCGCGAGAACACTTTACAACGACGAGGAGATTCGTTTCCAAACCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              421 AIGACTCIGCAAGCCTIGCIGGICCAAGIGCAAIAIGIAATITAIAAAIAITAIAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          481 AAGAGCCTATCAATGTATCTTTTGTACAATATGTTGTAAAATGTAGGATAGGATAGCT
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                                                                                                                                                           CGTCCTGACCTTGGAGGTGCGAGTCTGGGAAAGGCGCGCTCCCGGGGGGA-GCGGGCCCC
                                                                                                                                                                                                                                                                                                    GGAGATCAATTGTACTTACAAAGATTCCCATCTATTTAACTTTAACTTCTACCGTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABL65935 standard; DNA; 697 BP.
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20-SEP-2000; 2
20-SEP-2000; 2
20-SEP-2000; 2
20-SEP-2000; 2
22-SEP-2000; 2
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05-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a method (M1) for screening for an antineoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in to be tested for anti-neoplastic activity, determining a change in comprises a sequence (S) selected from 847 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarinoma, carcinoma, clear cell cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 739
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 620 TGGACACGCTCAGGCTGCCGTCCAGCTACATCGCCCACTTGAGGCAGATCCTGGCTAACG 679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             680 ACAAATACGAGAACGGGTACATTCACCCGGTCAACCTGACGTGGCCCTTTATGGTGGCCG
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Pred. No. 2.8e-124;
0; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 697 BP; 190 A; 164 C; 156 G; 180 T; 0 U; 7 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ebner R, Endress G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 3856; 44pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carter KC,
                                                                    2000US-0235711P.
2000US-0235720P.
2000US-0235840P.
2000US-0235863P.
2000US-0236028P.
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2000US-0236033P
2000US-0236034P
2000US-0236109P
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2000US-0237294P.
2000US-0237295P.
2000US-0237316P.
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Matches 621; Conservative
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26-88PP-2000;
27-88PP-2000;
27-88PP-2000;
27-88PP-2000;
28-88PP-2000;
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The present invention describes a method (M1) for screening for an antineoplastic agent. The method involves exposing cells to a chemical agent to be tested for antineoplastic activity, determining a change in comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in qene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the agent. M1 can be used in the treatment of cancer such properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidhey, prostate or pancreatic cancer, adilitrating lobular cancer, squamous call carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 581; DB 6; Length 697; Pred. No. 2.8e-124; O; Mismatches 27; Indels
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             25-SEP-2000; 2000US-0235134P.
26-SEP-2000; 2000US-0235280P.
26-SEP-2000; 2000US-0235280P.
27-SEP-2000; 2000US-023563P.
27-SEP-2000; 2000US-023563P.
27-SEP-2000; 2000US-023540P.
28-SEP-2000; 2000US-023603P.
29-SEP-2000; 2000US-0237173P.
02-OCT-2000; 2000US-0237294P.
03-OCT-2000; 2000US-0237294P.
03-OCT-2000; 2000US-0237294P.
03-OCT-2000; 2000US-0237294P.
03-OCT-2000; 2000US-0237568P.
03-OCT-2000; 2000US-0237568P.
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Local Similarity 95.1%;
les 621; Conservative C
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Soppet DR,
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680 ACAAATACGAGAACGGGTACATTCACCCGGTCAACCTGACGTGGCCCTTTATGGTGGCCG 739

TGGACACGCTCAGGCTGGCGTCCAGCTACATCGCCCACTTGAGGCAGATCCTGGCTAACG 1 TGGACACGCTCAGGCTGGCGTCCAGCTACATCGCCCCACTTGAGGCAGATCCTGGCTAACG

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ACAAATACGAGAAACGGGTACATTCACCCGGTCAACCTGACGTGGCCCTTTATGGTGGCCCG
                                                               121 GGAAACCCCAGAGAGCCTGAAAGAAGTGGTGGTGCCGCGAGCCGCGTTATGTGGAACCACCG
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05-JUN-2001; 2001US-00873319
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The invention relates to a method of diagnosing (I) the onset or progression of benign prostatic hyperplasia (BPH), or screening (II) for or infantifying an agent that modulates the onset or progression of BPH.

The method is based on changes in gene expression in BPH tissue isolated from patients exhibiting different clinical states of prostate (I) comprises the expression levels of normal prostate tissue. (I) comprises detecting the expression levels of one or more genes in prostate cells from the subject that are differentially regulated compared to normal prostate cells. (II) comprises preparing a first gene expression profile of prostate cells. (II) comprises preparing a first gene expression profile of prostate cells. (II) comprises preparing a first gene expression profile of substitution of BPH cells or BPH-like cell population, exposing the cells to the agent exposed cells, and comparing the first and second gene expression profiles. (I) is useful for diagnosing the first and second gene expression of BPH. The methods are useful to present information identifying the expression of given in the specification in the tissue or cells to the level of expression level in BPH. Agent expression level of genes of the last no gene in the database, and displaying the expression level of prostate cancer. ABK64106-ABK64860 represent human benign prostatic hyperplasia gene sequences of the invention
                                                      Disclosure; Page 367; 444pp; English.
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Sequence 697 BP; 190 A; 164 C; 156 G; 180 T; 0 U; 7 Other;

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Score 581; DB 6; Length 69
Pred. No. 2.8e-124;
0; Mismatches 27; Indels
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Best Local Similarity 95.1%;
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Claim 1; SEQ ID NO 1307; 2922pp; English.

diseases

The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP4328) and to cDNAs encoding them (ABC\$4131-ABC\$5305), and also encompasses polypeptides 90% identical and polynucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigens to polynucleotides, antibodies and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumnours of ovarian or orders norders such conditions include ovarian cancer, and breast cancer, and disorders (e.g., infertility, disorders of pregnancy, anovulation, clisorders, infections (e.g., chlampadia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, ophoritis and vaginatials), inflammatory conditions (e.g., mastitis, ophoritis and immunodeficiencies, autoimmune cophoritis, systemic lupus erythematosus), blood-related disorders, or anaemia), cardiovascular disorders and urinary system disorders. Ovarian antigen polypeptides and polymucleotides may also be used in screening for compounds which cutcher be used for gene therapy, chromosome mapping, in the identification of individuals and in forensic analysis, and the

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Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological
                                                                                                                                                                                       Human, ovarian antigen, ovary, ovarian; breast, cancer, tumour, ovarian cancer, breast cancer; tumour, reproductive system disorder; infertility, pregnancy disorder, anovulation, polycystic ovary syndrome, PCOS; ovarian cyst, dysmenorrhoea, endocrine disorder, infection; inflammatory condition; immune disorder; blood disorder, cardiovascular disorder; respiratory disorder; neurological disorder;
                                                                                                                                                                                                                                                                   gastrointestinal disorder; urinary system disorder; drug screening; gene therapy, chromosome mapping; forensic analysis; and antibody preparation; cyrostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive; gene; ss.
598 -agrirgcacrifitgaaaraaaccricfitaraficcraaaaaaaaaaaaaaga 649
                                                                                                                                                                Human ovarian antigen HNOJI85 cDNA, SEQ ID NO:1307.
                                                                                     BP.
                                                                                     ABQ55427 standard; cDNA; 632
                                                                                                                                                                                                                                                                                                                                                                                                              07-JUN-2001; 2001WO-US018569.
                                                                                                                                                                                                                                                                                                                                                                                                                                       07-JUN-2000; 2000US-0209467P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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30-MAY-2001; 2001WO-US010838

WO200194629-A2

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polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present sequence represents cDNA encoding a human ovarian antigan of the present invention. Note: The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                    41.3%; Score 525.6; DB 6; Length 632; 93.4%; Pred. No. 1.8e-111;
                                                                                                       Sequence 632 BP; 145 A; 176 C; 201 G; 93 T; 0 U; 17 Other;
                                                                                                                                                                    36; Indels
                                                                                                                                                  Pred. No. 1.8e-111;
0; Mismatches 36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Horrigan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 4458; 44pp; English.
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                                                                                                                      05-JUN-2000) 2000US-0209473P.
18-SEP-2000) 2000US-0233133P.
18-SEP-2000) 2000US-0233133P.
20-SEP-2000) 2000US-023403P.
20-SEP-2000) 2000US-0234034P.
20-SEP-2000) 2000US-0234034P.
22-SEP-2000) 2000US-0234509P.
25-SEP-2000) 2000US-0234567P.
25-SEP-2000) 2000US-0234567P.
25-SEP-2000) 2000US-0234567P.
25-SEP-2000) 2000US-0234567P.
25-SEP-2000) 2000US-023588P.
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26-SEP-2000) 2000US-023588P.
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27-SEP-2000) 2000US-023588P.
28-SEP-2000) 2000US-023588P.
29-SEP-2000) 2000US-023588P.
29-SEP-2000) 2000US-023588P.
29-CCT-2000) 2000US-023588P.
20-CCT-2000) 2000US-023789P.
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01-NOV-2000;
01-NOV-2000;
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Soppet DR,
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аn

Human; cancer; colon; breast; ovary; ossophagus; kidney; thyroid; stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous; cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma; gene; ds.

Lung cancer related gene sequence SEQ ID NO:4458.

(first entry)

15-MAY-2002

20-SEP-2000; 22-SEP-2000; 22-SEP-2000; 22-SEP-2000; 25-SEP-2000; 25-SEP-2000; 2

25-SEP-2000;

-SEP-2000;

27-SEP-2000;

28-SEP-2000;

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Pred. No. 8.7e-98;
0; Mismatches 3; Indels 0;
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                                                                                                                                                      Sequence 471 BP; 142 A; 89 C; 110 G; 130 T; 0 U; 0 Other;
                                                                                                                                                                                    Query Match
Best Local Similarity 99.4%;
Matches 468; Conservative
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stomach, lung; prostate; pancreas; carcinoma; antitumour; cancerous; cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                                                                      Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
                                                                                  Lung cancer related gene sequence SEQ ID NO:3908
         ABL65571/c
ID ABL65571 standard; DNA; 471
                                                            (first entry)
                                                                                                                                                                              WO200194629-A2
                                                                                                                                                          Homo sapiens
                                                            15-MAY-2002
                                        ABL65571;
                                                                                                                                     gene; ds
RESULT 7
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05-JUN-2000; 2000US-0209473P, 05-JUN-2000; 2000US-0209531P 30-MAY-2001; 2001WO-US010838

13-DEC-2001

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The present invention describes a method (M1) for screening for an antineoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in comprises a sequence (S) selected from 8447 sequences (st. where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocationma, carcinoma, clear cell cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
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                                     200005-02345034

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01-NOV-2000; 2000US-0245084P
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Weaver Z;
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                                                                                                                                351 AATGCTCCTCTCTCTGTCCCCCCCGCGAGAACACCATTTACAACGAGGAGATTCGTTT
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                           Gaps
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                          Indels
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        DB 6;
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       Score 466.2; DB 6,
Pred. No. 8.7e-98;
0; Mismatches 3;
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       Query Match
Best Local Similarity 99.4%;
Matches 468; Conservative
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(NISB ) JAPAN TOBACCO INC.
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The invention relates to a method of diagnosing (I) the onset or progression of benign prostatic hyperplasia (BPH), or screening (II) for or identifying an agent that modulates the onset or progression of BBH.

CC The method is based on changes in gene expression in BPH tissue isolated from patients exhibiting different clinical states of prostate

CC The method is based on changes in gene expression in BPH tissue isolated comparated to normal prostate tissue. (I) comprises compared to normal prostate tests in prostate cells from the subject that are differentially regulated compared to normal prostate cells. (II) comprises preparing a first gene expression profile co f BPH cells or BPH-like cell population, exposing the cells to the agent, preparing a second gene expression profile of the agent exposed cells, and comparing the first and second gene expression of BPH. (II) is useful confenting an agent that modulates the onset or progression of BPH. (IC) is useful confentifying an agent that modulates the onset or progression of genes cells, in a tissue or cells, by comparing the expression level of genes confent in the database, and displaying the expression level of expression of gene in the database, and displaying the expression level confent least one gene in the tissue or cells to the level of expression level in BPH. Agents using (II) are useful for treating BPH or prostate cancer. ABK64106-ABK64860 represent human benign prostatic confenting programment of the prostatic confenting manual programment or prostatic confenting manual programment or confenting manual programment or confenting manual programment or confenting manual prostatic confenting manual programment or confenting manual prostatic confenting manual programment or confenting manu
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Pred. No. 8.7e-98;
0; Mismatches 3;
Disclosure; Page 77; 444pp; English.
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Best Local Similarity 99.4%;
Matches 468; Conservative
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ACH23969
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Human adult ovary cDNA #2349.

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295 TCCTCTCTCTCCCCCCCCCCCCGCGAGACACTTTACAACGACGAGGAGATTCGTTTCCAAA 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 9069; 44pp; English.
                                                                                                                                                                      TAGATAAGAGCCTATCAAT 1112
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STACHE-CRAIN B
DICKSON M C.
JONES L W.
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LABAT I.
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(DICK/)
(JONE/)
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(LABA/)
                                                                                                                                                                                                                                                            RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated polynuclectide comprising any one of 38043 CDNA sequences, appearing as ACH12789-ACH5081, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynuclectide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (BST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing bloidiversities, or in identifying mutations responsible for generic disorders and other traits. The nuclectide sequences are also useful as hybridisation probes, as oligomers for PCR, for knownscene and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNM. The purified polypeptide is useful for generating antisense DNA or RNM. The purified polypeptide is useful for generating antisense DNA or RNM. The purified polypeptide is one of the 38043 isolated CDNA/EST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at
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                                                                                                                                                                                                                                                                                                                                                                                                                polynucleotide sequences obtained from various cDNA libraries, useful
                   ss, sequencing by hybridisation, SBH; expressed sequence tag; EST; mapping; biodiversity; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                 hybridization probes, as oligomers for PCR, for chromosome and gene
oping, in the recombinant production of protein, or in generating
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2.2e-90;
nes 3;
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99.3%; Pred. No. 2.2e
:ive 0; Mismatches
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STACHE-CRAIN E
DICKSON M C.
JONES L W.
                                                                                                                                                                                                                                                                                                                                               Labat I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or RNA
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                                                                      Homo sapiens,
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(STAC/)
(DICK/)
(JONE/)
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genome
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The invention relates to an isolated polynucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH5081, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polyapeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences of are useful in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide corresponsible for genetic disorders and other traits. The nucleotide corresponse and gene mapping, in the recombinant production of for chromosome and gene mapping, in the recombinant sequence correction, or in generating antisoense by or RNA. The purified polypeptide correction, or in generating antibodies specific for it. The present sequence is one of the 38043 isolated CDNA/RST sequences. Note: The sequence data correction of the printed specification, but was considered in electronic format directly from USPTO at correction, correctly from USPTO at correctly and correctly from USPTO at correctly and correctly from USPTO at correctly and correctly from USPTO at correctly correctly and correctly from USPTO at correctly from USPTO at correctly and correctly and correctly from USPTO at correctly and correctly from USPTO at correctly and correctly from USPTO at correctly and correctly 1093 CCAGAGGAGATCAATTGTACTTACAAAGATTCCCATCTATTTAACTTTAACTTTAACTTCTAC 1033 414 useful 415 ceresargacrerecasecerrecreserecaserecas aratrarararararara 474 EST; Human, 88; sequencing by hybridisation; SBH; expressed sequence tag; genome mapping; biodiversity; genetic disorder. " polynucleotide sequences obtained from various cDNA libraries, u hybridization probes, as oligomers for PCR, for chromosome and ge pping, in the recombinant production of protein, or in generating 3 Jones

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derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Classifying an ovarian tumor as a BRCA-1-like or BRCA-2-like or non-BRCA-like tumor by determining a pattern of expression in the ovarian tumor of
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAACTCCAGCTCCCAGCAGGAGGTGGCTGCGCCACACTCGGGAGGCCTCTTGGTTTCAGG 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ovarian cancer-related DNA #218 with altered ovarian cancer expression.
                                                                                                                                                                                                                                                                                                                                         CTCGGGGTTCCTTCTCACAACTCTGCGAAGGGGAAAGGGTTGTGAGACCCAACCAGACCC
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                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jene; ovarian tumor; BRCA-1-like; BRCA-2-like; non-BRCA-like; expression; primer; cancer.
                                                                                                                                                                                                                             0;
                                                                                                                                                                                     Score 246.8; DB 3; Length 271; Pred. No. 3.9e-47; 1; Mismatches 3; Indels 0;
                                                                                                                                                      Sequence 271 BP; 41 A; 97 C; 65 G; 67 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 233; 137pp; English.
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Best Local Similarity 98.4%;
Matches 248; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranalated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences
                                                                                                                                                                                                                                                                                            GCGTCCAGCTACATCGCCCACTTGAGGCAGATCCTGGCTAACGACAAATACGAGAAACGGG
                                                                                                                                                                                                                                                                                                                                                                       TACATTCACCCGGTCAACCTGACGTGGCCCTTTATGGTGGCCGGGAAACCCGGGAGAGTGAC
                                                                                                                    517 GCCAACGCGCGGAGCGGGCCCGCAIGCGAGTGCIGAGCAAGGCCTICTCCAGACTCAAG
                                                                                                                                                                                           ACCACCCTGCCCTGGGTGCCCCCCGACACCTCTCCAAGCTGCACACGCTCAGGCTG
                                                                                                                                                                                                                               GCGTCCAGCTACATCGCCCACTTGAGGCAGATCCTGGCTAACGACAAATACGAGAACGGG
                                                                                                                                                                                                                                                                                                                                           TACATTCACCCGGTCAACCTGACGTGGCCCTTTATGGTGGCCGGGAAACCCCGAGAGTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                      CTGAAAGAAGTGGTGACCGCGAGCCGCTTATGTGGAACCACCGCGTCCTGACCTTGGAGG
                                                                                                                                                      New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.
                                                                                Gaps
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                                           Length 482;
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                                                                               Indels
       Seguence 482 BP; 99 A; 156 C; 143 G; 83 T; 0 U; 1 Other;
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                                                                               5
                                           DB 9;
                                         Score 297.2; DB 9
Pred. No. 1.1e-58;
0; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human secreted protein 5' EST, SEQ ID NO: 12335.
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                                         23.4%;
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                                                             Best Local Similarity 97.1
Matches 302; Conservative
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RESULT

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pattern of expression in the ovarian tumor of several markers given in the specification; and (2) comparing a similarity of the pattern of expression of the markers in the ovarian tumor to a pattern of expression of the markers in a comparison tissue of a known BRCA-1-like or BRCA-2-like or non-BRCA-1ike tumor. The method is useful for classifying an ovarian tumor as a BRCA-1-like or BRCA-2-like or non-BRCA-like tumor. This sequence corresponds to an ovarian cancer -related gene having an altered pattern of expression in ovarian cancer. (Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                              146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         detection; cancer; cytotoxic; anticancer; cytostatic; gene therapy; ds;
                                                                                                                                                                                                                                                  265 TACAAAGATTCCCATCTATTTAACTTTATTAACTTCTACCGTGAAATGACTTGCAAGCC
                                                                                                                                                                                                                                                                                     TTGCTGGTCCAAGTGCAATATGTAATTATAAATATAAATAGATAAGAGCCTATCAATG
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                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                         5;
                                                                                                                                                                                 DB 10; Length 265;
                                                                                                                                                                    Score 236.2; DB lu;
Pred. No. 1.1e-44;
-red 3; Indels
                                                                                                                                                       Sequence 265 BP; 98 A; 33 C; 38 G; 96 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                           ATTTATAAAGTAATTCACTTAAAGATATATATTT
                                                                                                                                                                                              Pred. No. 1.1e
0; Mismatches
                                                                                                                                ftp.wipo.int/pub/published_pct_sequences).
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                                                                                                                                                                                 18.6%;
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ADM32307 standard; DNA; 265
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ZH GAN KENKYUKAI.
                                                                                                                                                                             Query Match
Best Local Similarity 98.1
Matches 260, Conservative
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specification
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The invention relates to a novel method for detecting cancer. The novel method involves measuring the expression level of a polypeptide encoded by a DNA having a sequence chosen from 119 fully defined sequences such as 416, 265, 456, 376, 360, 245, 280, 288, 221, 391 nucleotides etc., as given in the specification, or a DNA that hybridizes to the above DNA. Under stringent conditions. The invention further relates to: a diagnostic test of cancer, a DNA which encodes a cytotoxic protein and is coupled with a functional promoter region of a cancer detecting DNA; a cettor having cytotoxic DNA inserted in it; a transformed cell containing the staid vector; a method for evaluating the presence or absence of anticancer activity in a test sample; and producing a composition, by mixing a sample evaluated by the anticancer activity detection method and a carrier. The novel polynucleotides have cytostatic activity. The vector containing a cytotoxic polynucleotide can be used to treat cancer by gene therapy. The novel method of the invention allows early detection of cancer. This polynucleotide represents one of the 119 DNA sequences useful in the method for detecting cancer of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        265 TACAAAGATTCCCATCTATTTAACTTTATTAACTTCTACCGTGAAATGACTCTGCAAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       995 TACAAAGATTCCCATCTATTTAACTTTATTAACTTCTACCGTG-AATGACTCTGCAAGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18.6%; Score 236.2; DB 12; Length 265; 98.1%; Pred. No. 1.1e-44; cive 0; Mismatches 3; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 265 BP; 98 A; 33 C; 38 G; 96 T; 0 U; 0 Other;
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Best Local Similarity 98.1'
Matches 260, Conservative
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polymuclectide probes comprising a sequence selected from one of the 1490 comprised mentioned in the specification. The combination is useful as an array element in a microarray for monitoring the expression of a number of target polymuclectides. The microarray is particularly useful in the fagnosis and treatment of cancer and immunopathology and neuropathology. The microarray is useful in diagnostics and treatment regimens, drug discovery and development, toxicological and carcinogenicity studies, of prensics and pharmacogenomics. The microarray is also useful for monitoring progression of diseases and tore developing sophisticated profiles for the effects of currently available therapeutic drugs. The combination is also useful for purifying a suppopulation of mRNAs, cDNAs and genomic fragments and in research and diagnostic applications. The array can detect changes in expression in a large number of genes coding compination is algoraling pathway populations which can be used to diagnose various diseases including cancer e.g. adenocarcinoma and leukaemia, immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease can part disease. The present sequence represents a polymuclectide probe of the invention. Note: The sequence attention and lectronic form part of the printed specification but was obtained in electronic contact directly from USPPO at the sequence data for this patent in the contact of the printed specification but was obtained in electronic contact.
                                                     Combination of polynucleotide probes, useful as array elements in microarray for monitoring the expression of a number of target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seqdata.uspto.gov/sequence.html?DocID=06500938B1
                                                                                                                                                                            Claim 1; SEQ ID NO 1028; 65pp; English.
WPI; 2003-352189/33
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Sequence 240 BP; 55 A; 83 C; 72 G; 27 T; 0 U; 3 Other;

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                                                                                    448 AAGGCGCCCACCAAGAAGAGCCCCCTGAGCGGGGTCAGCCA-GGAGGGGAAGCAGGTCCA
                                                                                                               GCGCAACGCCGCCAACGCGCGAGAGC-GGGCCCGCATGCGAGTGCTGAGCAAGGCCTTCT
                                                                                                                                                                                                             61 GCGCAACGNCGCCAACGCGGCGGGGCCCCGCATGCGAGTGCTGAGCCAAGGCCTTCT
                                            Gaps
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16.7%; Score 213; DB 10; Length 240; 97.9%; Pred. No. 2.5e-39; Live 0; Mismatches 3; Indels
                        Best Local Similarity 97.9
Matches 235; Conservative
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Human; probe; ss; receptor-like polypeptide; transducing polypeptide; defector-like polypeptide; cancer; immunopathology; neuropathology; development; toxicology; carcinogenicity; signalling pathway polypeptide; adrenal gland; bladder; bone; signalling pathway polypeptide; adrenal gland; bladder; bone; bone marrow; brain; breast; cervix; tumouropathology; AIDS; diabetes; pancreatitis; osteoporosis; ulcerative colitis; neuropathology; dementia; amnesia; epilepsy; Alzheimer's disease; depression.
                                                                                                                                                                                              Human polynucleotide probe #1028.
                                                  ADIS6226 standard; DNA; 240
                                                                                                                                                 (first entry)
                                                                                                                                              22-APR-2004
                                                                                                ADI56226;
RESULT 15
AD156226
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XX
XX
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XX
KW Human
XW effec
KW drug
KW signa
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KW signa
KW diabe
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Homo sapiens

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The invention relates to a composition of polynucleotide probes comprising at least a portion of a gene encoding a receptor-like polyapetide, second polynucleotide probes comprising at least a portion of a gene encoding an effector-like polypeptide. The probes of the composition are useful as array elements in a microarray for monitoring the expression of target polynucleotides. The microarray is useful in the clauropathology. It can also be used for drug discovery and development, toxicological and carcinogenicity studies, forensics or pharmacogenomics. Microarrays can also be used for monitoring the progression of diseases that may be associated with the altered expression of signalling pathway polypeptides. The composition can also be used to purify a subpopulation of max may be associated with the altered expression of signalling pathway polypeptides. The composition can also be used to purify a subpopulation of max and treatment of cancer, e.g. cancers of max also useful for the diagnosis and treatment of cancer, e.g. cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast or cervix, an immunopathology, e.g. dementia, amnesta, chis patent did not form part of the printed specification but was contained in electronic forme part of the printed specification but was contained in the printed specification but was
                                                                                                                                                                                                                                                                                                                                 New composition comprising polynuclectide probes, useful as array elements in a microarray for monitoring the expression of target polynuclectides or purifying a subpopulation of mRNAs, cDNA, or genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          448 AAGGCGCCCACCAAGAAGAACCCCCTGAGCGGGGTCAGCCA-GGAGGGGAAGCAGGTCCA
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                                                                                                          26-NOV-2002; 2002US-00305720
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                                                               15-JAN-2004
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626 CGCTCAGGCTCCAGCTACATCGCCCACTTGAGGCAGATCCTGGCTAACGACAAAT 181 CGCTCAGGCTGGCCTCCAGNTACATNGCCCACTTGAGGCAGATCCTGGCTAACGACAAT Search completed: December 16, 2004, 17:30:53 Job time : 687 secs

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Sequence 1028, Ap
Sequence 116, Appl
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-800-353-49

US-08-800-353-49

US-08-96-45-641-120

US-08-96-76185-49

US-08-96-76185-49

US-08-96-761-120

US-08-96-76-120

US-08-98-120

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US-08-98-120

US-08-52-142A-10

US-08-53-155A-14

US-09-636-215-736

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      507 GCGCAACGCCGCCAACGCGCGAGAGC-GGGCCCGCATGCGAGTGCTGAGGCAAGGCCTTCT 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                566 CCAGACTCAAGACCACCCTGCCCTGGGTGCCCCCGACACCCAAGCTCTCCAAGCTGGACA 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 ccadacticaadaccaccerdecerdecececececeacacereceaacereceaacerdeaca 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     626 CGCTCAGGCTGGCGTCCAGCTACATCGCCCACTTGAGGCAGATCCTGGCTAACGACAAAT 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGCTCAGGCTGGCGTCCAGNTACATNGCCCACTTGAGGCAGATCCTGGCTAACGACAAAT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GCGCAACGNCGCCAACGCGCGAGAGCGGGGCCCGCATGCGAGTGCTGAGCAAGGCCTTCT
                        Sequence 1028, Application US/09016434 | 02.4 C | Defect. 10 Betent No. 6500938 | General Information: Application of Sequence 1028. Application: Application: Applicant: Jeffrey J. Seilhamer TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING TITLE OF INVENTION: PATHWAY GENE EXPRESSION NUMBER OF SEQUENCES: 1490 | CORRESPONDENCE ADDRESS: ADDRESSEE: INCYTE PHARMACEUTICALS, INC. STREET: 3174 FORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
16.7%; Score 213; DB 4; Length 240;
Best Local Similarity 97.9%; Pred. No. 1.7e-43;
Matches 235; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: 97,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1028:
SEQUENCE: CHRACTERISTICS:
LENGTH: 240 base pairs
FYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIBRARY: KIDNNOTOS;
CLONE: 954226
US-09-016-434-1028
                                                                                                                                                                                                                                                                                   CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: line IMMEDIATE SOURCE
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RESULT 3 US-09-771-357-106

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PARTERIA NO. 6756200
GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
APPLICANT: SUKUMAR, SATASWALI
APPLICANT: EVRON, BILA
APPLICANT: DAVIDSON, Nancy
FILLE REFERENCE: JUHISA
APPLICANT: APPLICATION WUMBER: US/09/771,357
CURRENT APPLICATION WUMBER: US/09/771,357
CURRENT FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 110
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 106
LENGTH 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1502 AGTCGCTGAACGAGGCGTTCGCCGCTGCGGAAGATCATCCCCCACGCTGCCCTCGGA-- 1559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1560 -CAAGCTGAGCAAGATTCAGACCCTCAAGCTGGCGGCCAGGTACATCGACTTCCTCTACC 1618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1442 CTTACGAĞĞAĞCTĞCAĞACĞCĞĞĞTČATĞĞCCAACĞTĞCĞĞĞĞAĞCĞCCAĞĞĞĞACCÖ 1501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              425 GCGGCGGCCTGGGCAAGAGGAGGAGGCGCCCACCAAGAAGAGCCCCCCTGAGCGGGGTCA 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  545 GAGTGCTGAGCAAGGCCTTCTCCAGACTCAAGACCACCCTGCCCTGGGTGCCCCCGGACA 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      605 CCAAGCTCTCCAAGCTGGACACGCTCAGGCTGCGGCTCCAGCTACATCGCCCACTTGAGGC 664
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Sequence 11, Application US/07891942G

Sequence 11, Application US/07891942G

Patent No. 5579511

GENERAL INFORMATION:

APPLICANT: Kwon, Byoung Se

TITLE OF INVENTION: A REGULATORY PROTEIN IN THE MELANIN PROTEIN PATHWAY

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Christopher A. Michaels, Barnard, Brown &

ADDRESSEE: Michaels

STREET: 306 East State Street, Suite 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          485 GCCAGGAGGGGAAGCAGGTCCAGCGCAACGCCGACGCGCGGGGCGGCCCGCATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

5.6%; Score 71.8; DB 4; Length 1800;
Best Local Similarity 57.5%; Pred. No. 4.7e-08;
Matches 149; Conservative 0; Mismatches 107; Indels 3
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COMPUTER READABLE FORM:
MEDIUM TYPE: Rloppy disk
COMPUTER: IBM PC compatible
COMPTITE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Ralease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/891,942G
FILING DATE: 01-UW-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/915,753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1619 AGGTCCTCCAGAGCGACGA 1637
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ORGANISM: Homo sapiens
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Gaps

260

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Sequence 12, Application US/08910973
Patent No. 5795723
Patent No. 5795723
APPLICANT: Tapscott, Stephen J.
APPLICANT: Tapscott, Stephen J.
APPLICANT: Olson, James M.
TITLE OF INVENTION: Expression of Neurogenic bHLH Genes in Primitive Neuroectoder NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Christensen O'Connor Johnson KindnessPLLC
STREET: 1410 Fifth Avenue, Suite 2800
CITY: Seatle
STREET: MA
                                                                                                                                                                                                                                                            178 Addecededa Adda Adda Tarcada de Comanderior en contrar en contrar en 119
                                                                                                                                                                                                                 141 AGGIGGCIGCGCACACICGGGAGGCCICIIGGIIICAGGGICTCICICICICICICICTCICIC
                                                                                                                                                                                                                                                                                                            0;
                                                                                                                 Query Match 5.0%; Score 63.4; DB 1; Length 305; Best Local Similarity 64.8%; Pred. No. 2.4e-06; Matches 94; Conservative 0; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NOMBER: US/06/910,9/9
CLASSIFICATION 1435
PRIOR APPLICATION NUMBER: US 08/239,238
FILING DATE: 06-MAY-1994
PRIOR APPLICATION NUMBER: WS 08/239,238
FILING DATE: 06-MAY-1995
FILING DATE: 08-MAY-1995
FILING DATE: 08-MAY-1995
FILING DATE: 08-MAY-1995
FILING DATE: 08-MAY-1995
APPLICATION NUMBER: PCT/US96/17532
FILING DATE: 30-OCtober-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sheiness, Diana K.
REGISTRATION NUMBER: 95.356
REFERENCE/DOCKET NUMBER: PCR-1-10958
TELECOMMULCATION NUMBER: 10-05-024-0735 (direct)
TELEPAX: 206-225-0779
INPORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1268 base pairs
TYPE: MUCLEIC acuble
TYPE: MUCLEIC acuble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER REARABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,973
                                                                                                                                                                                                                                                                                                                                                                                                            261 CCCAAACATGTCCACCGGCTCCCTC 285
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       STRANDEDNESS: single
                           TOPOLOGY: linear MOLECULE TYPE: cDNA US-08-253-155A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/08253155A
Sequence 4, Application US/08253155A
Sequence 4, Application US/08253155A
GENERAL INFORMATION:
APPLICANT: Gyuria, Jeno
SEQUENCES: 95
CORRESPONDENCE ADDRES: 95
CORRESPONDENCE ADDRES: 95
CONTY: Bostco
STATE: MA
COUNTY: USA
ZIP: 02109
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: AZCII(text)
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/253,155A
FILING DATE: US-OFTWATION:
NAME: Vincent, Matchew P.
REGISTRATION INFORMATION:
NAME: Vincent, Matchew P.
REFERRUCE/DOCKET NUMBER: 36,709
REFERRUCE/DOCKET NUMBER: MII-028
TELECHOMENICATION INFORMATION:
TELECHORTH: 305 base pairs
LYPE: nucleic acid
FILING DATE: 06-OCT-1986

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/362,847
FILING DATE: 07-UN-1989
ATTONEY/AGENT INFORMATION:
NAME: Michaels, Christopher A
REGISTRATION NUMBER: 34,390
REFRENCE/DOCKET NUMBER: INDI
TELECOMMUNICATION INFORMATION:
TELEPONE: 607-273-1711
TELEPAN: 607-273-1711
SEQUENCE CHARACTERISTICS:
LENGTH: 2397 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                167 CTCTTGGTTTCAGGGTCTCTCTGTCT
                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-891-942G-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1468 TCTGTGT 1462
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US-08-253-155A-4/c
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390 GGACGCACTGCGCAGCGTGCTGCCTCGTTCCCCGACGACACCAGCTCACCAAAATCGA 449
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                                                                                                                                                                                                                                                                                                                                                                                                                               504 CCAGCGCAACGCCGCCCAACGCGCGAGGCGGGCCCGCATGCGAGTGCTGAGCAAGGCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            624 CACGCTCAGGCTGGCGTCCAGCTACATCGCCCACTTGAGGCAGATCCTG 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       450 GACGCTGCGCTTCGCCTACAACTACATCTGGGCTCTGGCCGAGACACTG 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2245 Application US/09042353
Patent No. 6255458
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for INVENTION: Transgenic No. 6255458-Human Animals for TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for TITLE OF INVENTION: Producing Heterologous Antibodies NUMBER OF SEQUENCES: 421
CORRESPONDENCE ADDRESS:
ADDRESSED: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                           Query Match 5.0%; Score 63.4; DB 4; Length 1268; Best Local Similarity 60.9%; Pred. No. 4.8e-06; Matches 103; Conservative 0; Mismatches 66; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPENATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,353
FILING DATE: 13-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PELICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 26-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
PRIOR APPLICATION DATE: US 08/155,301
FILING DATE: 18-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/810,279 FILING DATE: 17-DEC-1991 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408 FILING DATE: 18-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION DATA:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-UUN-1992
APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
                                                                                                    CLONE: 20A1 (neuroD3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: CALL
COUNTRY: USA
TO 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      California
USA
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CLASSIFICATION:
                                                                                                                         FEATURE:

NAME/KEY:

LOCATION:

US-09-499-227-12
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Patent No. 644463
GENERAL INFORMATION:
APPLICANT: Tapscott, Stephen J.
APPLICANT: Olson, James M.
TITLE OF INVENTION: Expression of Neurogenic bHLH Genes in Primitive Neuroectoder
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                  563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      330 ccescecercaageccaacearcecaacecaacecarececaracracaarerreaacececer 389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       564 CTCCAGACTCAAGACCACCCTGCCCTGGGTGCCCCCGGACACCAAGCTCTCCAAGCTGGA
                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       624 CACGCTCAGGCTCCAGCTACATCGCCCACTTGAGGCAGATCCTG 672
                                                                                                                                                                                              Score 63.4; DB 1; Length 1268; Pred. No. 4.8e-06; 0; Mismatches 66; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Christensen O'Connor Johnson KindnessPLLC
STREET: 1420 Fifth Avenue, Suite 2800
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:

APPLICATION NUMBER: PAGENTE Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/499,227
FILING DATE: 05-August-1998
PRIOR APPLICATION NUMBER: US 08/239,238
FILING DATE: 06-May-1994
PRIOR APPLICATION NUMBER: WO PCT/US95/05741
PLING DATE: 06-May-1995
PRIOR APPLICATION NUMBER: PCT/US96/17532
PILING DATE: 00-Coccober-1996
PRIOR APPLICATION NUMBER: US 08/910,973
PILING DATE: 07-August-1997
APPLICATION NUMBER: US 08/910,973
FILING DATE: US 08/910,973
FIL
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEC ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1268 base pairs
                                                                                                                                                                                       Query Match
Best Local Similarity 60.9%;
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA (genomic)
CLONE: 20Al (neuroD3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 98101-2347
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                             55..768
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                                                          ) NAME/KEY:
; LOCATION:
US-08-910-973-12
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US-09-499-227-12
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                               FEATURE
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5.0%; Score 63.2; DB 3; Length 3618;
Best Local Similarity 67.4%; Pred. No. 9e-06;
Matches 89; Conservative 0; Mismatches 43; Indels 0
                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: RIOPRY disk
COMPUTER: INDAYC Compatible
CORPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,417A
FILING DATE: 02-Dec-1996
CLASSIFCATION: CURKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/54,404
FILING DATE: 10-OCT-1996
APPLICATION NUMBER: US 08/52,322
FILING DATE: 00-DEC-1994
APPLICATION NUMBER: US 08/35,322
FILING DATE: 09-MAR-1994
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/165,301
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1993
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1993
APPLICATION NUMBER: US 07/990,860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Serafini, Andrew T.
REGISTRATION NUMBER: 41,303
REFERENCE/DOCKET NUMBER: 014643-009030US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 1..3618
; CTHER INFORMATION: /note= "vector pGPe";
; SEQUENCE DESCRIPTION: SEQ ID NO: 72:
US-08-758-417A-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 3618 base pa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: singl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAACATGTCCAC 275
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Patent No. 6300129
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , 0
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ADDRESSEB: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 63.2; DB 3; I
Pred. No. 9e-06;
0; Mismatches 43;
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
PRIOR APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
PRIOR APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-WAR-1994
PRIOR APPLICATION NUMBER: US 08/352,322
FILING DATE: 09-WAR-1994
PRIOR APPLICATION DATA: WO 8/352,322
FILING DATE: 09-WAR-1994
PRIOR APPLICATION DATA: WO 8/352,322
FILING DATE: 09-WAR-1995
PRIOR APPLICATION DATA: WO 8/354,404
FILING DATE: 10-0CT-1995
PRIOR APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-0CT-1996
PRIOR APPLICATION NUMBER: US 08/758,417
FILING DATE: 10-0CT-1996
PRIOR APPLICATION NUMBER: WO PCT/US97/21803
FILING DATE: 10-0CT-1996
PRIOR APPLICATION NUMBER: WO PCT/US97/21803
FILING DATE: 10-DEC-1997
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: WO PCT/US97/21803
FILING DATE: 02-DEC-1996
PRIOR APPLICATION NUMBER: O14643-009040US
FILING DATE: APPLICATION NUMBER: O14643-009040US
TELEPONE: APPLICATION NUMBER: O14643-009040US
TELEPONE: (415) 576-0200
INPORMATION POR SEQ ID NO: 224:
SEGUENCE CHARACTERISTICS:
LENGTH: 3618 DATE: DATE: LENGTH: 3618 DATE: DATE: LENGTH: 3618 DATE: LENGTH: LANGTH: AND LENGTH: LANGTH: LA
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Best Local Similarity 67.4%;
Matches 89; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                264 AAACATGTCCAC 275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-758-417A-72
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RESULT 12
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US-08-800-353-49
) Sequence 49, Application US/08800353
) Sequence 49, Application US/08800353
) Fatent No. 5874299
) GENERAL INFORMATION:
APPLICANT: Lonbergy Nils
) TITLE OF INVENTION: Transgenic No. 5874299-Human Animals Capable of TITLE OF INVENTION: Producing Heterologous Antibodies
) TITLE OF SEQUENCES: 77
CORRESPONDENCE ADDRESS: 77
) CORRESPONDEN
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US-07-834-539A-49
; Sequence 49, Application US/07834539A
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: Transgenic Non-Human Animals Capable of TITLE OF INVENTION: Producing Heterologous Antibodies
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS: 7
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/834,539A
FILING DATE: 1992-05
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 1464;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEPAX: 415-543-9603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 49: SEQUENCE CHARACTERISTICS: LENGTH: 3698 base pairs TYPE: nucleic acid combanded single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               204 TCTTCCTCGCTTTCTC
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Matches 89; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Length 3698;
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APPLICANT: Lonberg, Nils

APPLICANT: Lonberg, Nils

APPLICANT: Lonberg, Nils

TITLE OF INVENTION: Transgenic Non-Human Animals Capable

TITLE OF INVENTION: Producing Heterologous Antibodies

NUMBER OF SEQUENCES: 75

CORRESPONDENCE ADDRESS:

ADDRESSEE: William M. Smith

STREET: One Market Plaza, Steuart Tower, Suite 2000

CITY: San Francisco

STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 5.0%; Score 63.2; DB 2; Length 3
Best Local Similarity 67.4%; Pred. No. 9.1e-06;
Matches 89; Conservative 0; Mismatches 43; Indels
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Flam PC Compatible
OPERATION SYSTEM: PC-DCS/MS-DCS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,353
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: US/07/834,539
FILING DATE: 1992-02-05
ATTORNEY/AGENT INPORMATION:
NAME: Smitch, William M.
NAME: Smitch, William M.
NAME: Smitch, William M.
NAME: Smitch William M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06185
FILING DATE: 19910828
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 3698 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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TOPOLOGY: lir
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Patent No. 5719932
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5719032-Human Animals for INVERSE OF SEQUENCES: 150
CORRESPONDENCE: ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 63.2; DB 1; Length 3699;
Pred. No. 9.1e-06;
                                                                                                                                                                                                                                                                                      Length 3699;
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MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Elb PC compatible
COPERATIOS SYSTEM: PC-DCS/MS-DCS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-7UN 1992
ATTORNEY/AGENT INFORMATION:
NAME: SMITCH, William M.
REGISTRATION NUMBER: 30,223
REFRENCE/DCOKET NUMBER: 14643-000913
TFELECOMMUNICATION INFORMATION:
TELEBHONE: 415-326-2400
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                                                                                                                                                                                                                                                                                Query Match
5.0%; Score 63.2; DB 1;
Best Local Similarity 67.4%; Pred. No. 9.1e-06;
Matches 89; Conservative 0; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: William M. Smith
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
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INFORMATION FOR SEQ ID NO: 120:
SEQUENCE CHARACTERISTICS:
LENGTH: 3699 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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MOLECULE TYPE: DNA (genomic)
US-08-053-131-120
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   INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 3699 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity
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ZIP: 94111-3834
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US-08-053-131-120
US-08-053-131-120

Sequence 120, Application US/08053131

Sequence 120, Application US/08053131

Patent No. 5661016

GENERAL INFORMATION:
APPLICANT: Lonberg Nils

TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for TITLE OF INVENTION: Producing Heterologous Antibodies

VORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 200
CITY: San Francisco
STATE: California

CONTREY: USA
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MEDIUM TYPE:

COMPUTER READABLE FORM:

MEDIUM TYPE:

COMPUTER PERADABLE FORM:

MEDIUM TYPE:

COMPUTER FEADABLE FORM:

COMPUTER PERADABLE FORM:

COMPUTER PERADABLE FORM:

COMPUTER PERADABLE FORM:

COMPUTER PERADABLE PERADABLE

SCHORARE:

APPLICATION NUMBER:

CLASSIFICATION DATA:

APPLICATION NUMBER:

APPLICATION NUMBER:

CLASSIFICATION DATA:

APPLICATION NUMBER:

CAPPLICATION NUMBER:

APPLICATION NUMBER:

CAPPLICATION NUMBER:

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REGISTRATION NUMBER: 87654
REPERENDE/DOCKET NUMBER: 1464
TELEPHONE: 415-543-9600
FILEPHONE: 415-543-9603
FILEPHONE: 415-543-643
INPORMATION FOR SEQ ID NO: 8 SEQUENCE CHARACTERISTICS: LENGHH: 3698 base pairs TYPE: NUCLBIC ACID STRANDEDNESS: single TYPE: NUCLBIC ACID STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) PCT-US92-06185-49
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   0; Gaps
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US-07-853-408B-120
; Sequence 120, Application US/07853408B
; Patent No. 5789650
; GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: Che Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: Ush
APPLICANTON ARABABLE FORM:
MEDIUM TYPE: Loppy disk
COMPUTER: NUMBER: Us/07/853,408B
FILING DATE: 1992018
FILING DATE: 1992019
FILING DATE: 19
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   43; Indels
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INFORMATION FOR SEQ ID NO: 120:
SEQUENCE CHARACTERISTICS:
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TYPE: NUCLEIC ACID
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89; Conservative
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Search completed: December 16, 2004, 20:18:53
Job time : 135 secs
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Scoring table:

score:

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Aca56430 Chicken s
Ach25626 Human pol
Ach23969 Human adu
Aca50465 Human mus
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Aca7639 Drosophil
Ach10298 Drosophil
Aca29100 S. fradia
Aca2910 N. gonorr
Aca26168 Neisseria
Aca26108 Neisseria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein regulating gene expression PRGE-23 cDNA clone 3340296.
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ABN27386
ABL08723
ABL08723
ABZ188589
AAS76438
AAS12517
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AAS459100
AAS45090
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268. .807
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98US-0104624P.
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29-JUL-1998;
14-OCT-1998;
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-MODEL=frame+ p2n.mcdel -DEV=x1h

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-Q=/Gapt_1/GaPtO spool h/USO9701674/runat 15122004 100529 28299/app_query.fasta_1.327

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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=01igo -TRANS=human40.cdi

-LIST=K5 -DOCALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL

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-USER=USO9701674 @CGN 1 1 470 @runat 15122004 100529 28299 -NCPU=6 -ICPU=3

-NO_MAPP -LARGEQUERY -NGS SCORES=0 -MAIT -DSPBADCK=170 -LONGLOG

-DBT TIMEOUT=120 -WARN TIMEOUT=30 -THREADS 1 -XGAPEXT=60 -FGAPOP=6

-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELDEXT=7
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Ach21857 Human adu
Ab165519 Lung canc
Ab165935 Lung canc
Abk64784 Human ben
Abq55427 Human ova
                                                                                                                                   December 17, 2004, 00:04:02; Search time 455 Seconds (without alignments) 2065.157 Million cell updates/sec
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                                                                                                                                                                                                                                                      MSTGSLSDVEDLQEVEMLEC......PESDLKEVVTASRLCGTTAS 179
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                    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                               nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                  4134886 seqs, 2624710521 residues
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179
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Maximum DB seq length: 2000000000
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Command line parameters:

Database :

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Length DB

Query

Score

Result 8 697 697 697 632

100.0 52.5 34.1 34.1 24.1

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US-09-701-674A-23 (1-179) x ACH21857
                                                                       The present sequence is that of Incyte clone 3340296 encoding new human protein regulating gene expression PRGE-23 (see AAYS8630). The cDNA was initially isolated from spleen tissue cDNA library SPLNNOT10, and the full-length sequence assembled from overlapping clones from a number of libraries. PRGE-23 is expressed in reproductive, developmental and urologic tissues associated with cancer, inflammation and foctal diseases, disorders or conditions. It is characterised as an Myc-type HiH protein. The invention provides PRGE polypeptides (see AAYS8608-38) and polynucleotides (see AAZS7839-68), expression vectors, host cells, antibodies, agonists and antegonists. It also provides methods for diagnosing, treating or preventing disorders associated with expression of PRGE. Polynucleotides are also used as sources of probes and primers for diagnosis and monitoring of disease, also for detecting related sequences and in gene mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ArgAsnAlaAlaAsnAlaArgGluArgAlaArgMetArgValLeuSerLysAlaPheSer 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       328 gaccccricaaaargcariccaacaaccaarricrcactrccaaccaccaccaccaacaaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           448 AAGGGGCCCACCAAGAAGAGCCCCCTGAGCGGGGTCAGCCAGGAGGGGAAGCAGGTCCAG 507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GluSerAspLeuLysGluValValThrAlaSerArgLeuCysGlyThrThrAlaSer 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     388 AGCTCCAACTGCGAGAATGGGTCTCCCCAGAAGGGCCGCGGGGGGCTGGGGCAAGAGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AspGlyLeuLysMetAspSerAsnLysGluPheValThrSerAsnGluSerThrGluGlu
                                                                                                 New human polypeptides that regulate gene expression, for treatment, prevention and diagnosis of, e.g. cancer.
                        Corley NC
Lu DAM;
                                                                                                                                                                                                                                                                                                                                                         Sequence 1272 BP; 311 A; 358 C; 318 G; 285 T; 0 U; 0 Other;
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179
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                         Bandman O,
Patterson C,
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Matches:
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                        Hillman JL,
Baughn MR,
                                                                                                                                        Claim 9; Page 139; 150pp; English
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179.00
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(INCY-) INCYTE PHARM INC
                        Lal P, Yue H, Tang YT,
Guegler KJ, Gorgone GA,
                                                            WPI; 2000-116543/10.
P-PSDB; AAY58630.
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Best Local Similarity:
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The invention relates to an isolated polymucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polymucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (BST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, or chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. The purified polypeptide is useful for generating antisense DNA or RNA. The purified polypeptide is useful for generating antisense DNA or RNA. The purified polypeptide is useful for generating antisense specific for it. The present sequence is one of the 38043 isolated cDNA/BST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was contained in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating
                                                                                                                                                                                                                                                                                                                                                                                                              Human, ss, sequencing by hybridisation, SBH, expressed sequence tag; genome mapping, biodiversity, genetic disorder.
748 GAGAGTGACCTGAAAGAAGTGGTGACGCGGGAGCCGCTTATGTGGAACCACCGCGTCC
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Matches:
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                                                                                                                                                             ACH21857 standard; cDNA; 482
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LABAT I.
STACHE-CRAIN B.
DICKSON M C.
JONES L W.
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antisense DNA or RNA
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(STAC/)
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                                                                             145
                                                                                                                  HisProValAsnLeuThrTrpProPheMetValAlaGlyLysProGluSerAspLeuLys 165
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stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
AlaargGluargalaargMetArgValLeuSerLysAlaPheSerArgLeuLysThrThr
                                     LeuProTrpValProProAspThrLysLeuSerLysLeuAspThrLeuArgLeuAlaSer
                                                 CTGCCCTGGGTGCCCCCCGACACACTCTCCAAGCTGGACACGCTCAGGCTGGCGTCC
                                                                           SerTyr11eAlaHisLeuArgGln11eLeuAlaAsnAspLysTyrGluAsnGlyTyr11e
                                                                                                                                  CACCCGGTCAACCTGACGTGGCCCTTTATGGTGGCCGGGAAACCCGAGAGTGACCTGAAA
           GCGCGAGAGCGGGCCCGCATGCGAGGCTTGTTCCAGACCCTTCTCCAAGACCACC
                                                                                              AGCTACATCGCCCACTTGAGGCAGATCCTGGCTAACGACAAATACGAGAACGGGTACATT
                                                                                                                                                        GluvalvalThrAlaSerArgLeuCysGlyThrThrAlaSer 179
                                                                                                                                                                     GAAGTGGTGACCGCGAGCCGCTTATGTGGAACCACCGCGTCC 320
                                                                                                                                                                                                                                                                              cancer related gene sequence SEQ ID NO:3856
                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUN-2000; 2000US-0209473P.
18-SEP-2000; 2000US-0233113P.
18-SEP-2000; 2000US-0233113P.
20-SEP-2000; 2000US-023403P.
20-SEP-2000; 2000US-023403P.
22-SEP-2000; 2000US-023455P.
22-SEP-2000; 2000US-023455P.
25-SEP-2000; 2000US-023455P.
25-SEP-2000; 2000US-023456P.
25-SEP-2000; 2000US-023492P.
25-SEP-2000; 2000US-023456P.
25-SEP-2000; 2000US-023580P.
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25-SEP-2000; 2000US-023580P.
26-SEP-2000; 2000US-023580P.
27-SEP-2000; 2000US-023580P.
27-SEP-2000; 2000US-023580P.
27-SEP-2000; 2000US-023580P.
28-SEP-2000; 2000US-023583P.
28-SEP-2000; 2000US-023583P.
28-SEP-2000; 2000US-023583P.
28-SEP-2000; 2000US-023583P.
28-SEP-2000; 2000US-023583P.
28-SEP-2000; 2000US-0236033P.
28-SEP-2000; 2000US-0236033P.
                                                                                                                                                                                                                   ABL65519 standard; DNA; 697 BP.
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                                                                                                                                                                                                                                                           (first entry)
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The present invention describes a method (M1) for screening for an antineoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in comprises a sequence (S) selected from 8447 sequences (given in ABL61664 of ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, andenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set.
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 3856; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                          Carter KC,
02-OCT-2000; 2000US-0237278P.

02-OCT-2000; 2000US-0237294P.

02-OCT-2000; 2000US-0237316P.

03-OCT-2000; 2000US-0237316P.

03-OCT-2000; 2000US-0237316P.

03-OCT-2000; 2000US-0237609P.

03-OCT-2000; 2000US-0237606P.

03-OCT-2000; 2000US-0237606P.

01-NOV-2000; 2000US-024867P.

01-NOV-2000; 2000US-024867P.
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Weaver Z;
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Pred. No.:
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Soppet DR,
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158 122

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The present invention describes a method (M1) for screening for an antineoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in comprises a sequence (S) selected from 847 sequences (Siven in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gane therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarinoma, carcinoma, clear call cancinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's cell
ant to be tested for anti-neoplastic activity, and determining a change expression of a gene of a signature gene set.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 AspThrLeuArgLeuAlaSerSerTyrIleAlaHisLeuArgGlnIleLeuAlaAsnAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 GACACGCTCAGGCTGGCGTCCAGCTACATCGCCCACTTCAGGCAGATCCTGGCTAACGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              139 LysTyrGluAsnGlyTyrIleHisProValAsnLeuThrTrpProPheMetValAlaGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 AATACGAGAACGGGTACATTCACCCGGTCAACCTGACGTGGCCCTTTATGGTGGCCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LysProGluSerAspLeuLysGluValValThrAlaSerArgLeuCysGlyThrThrAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; benign prostatic hyperplasia; BPH; prostate cancer; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 697 BP; 190 A; 164 C; 156 G; 180 T; 0 U; 7 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                     Claim 1; SEQ ID NO 4272; 44pp; English
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                                                                                                                                                                                                     Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Endress G,
                                                                                                                                                             Lung cancer related gene sequence SEQ ID NO:4272.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carter KC,
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28-SEP-2000; 2000US-0236032P.
28-SEP-2000; 2000US-0236033P.
28-SEP-2000; 2000US-0236033P.
28-SEP-2000; 2000US-0236111P.
29-SEP-2000; 2000US-0236111P.
29-SEP-2000; 2000US-0236111P.
02-OCT-2000; 2000US-0237173P.
02-OCT-2000; 2000US-0237173P.
02-OCT-2000; 2000US-0237294P.
02-OCT-2000; 2000US-0237294P.
                                ABL65935 standard; DNA; 697 BP
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2000US-023313P.
2000US-0233133P.
2000US-0234017P.
2000US-0234034P.
2000US-0234034P.
2000US-0234034P.
2000US-0234034P.
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2000US-0234924P.
2000US-0235077P.
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2000US-0235134P.
2000US-0235280P.
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27-SEP-2000; 2000US-0235840P.
27-SEP-2000; 2000US-0235863P.
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27-SEP-2000; 2000US-0235711P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2001; 2001WO-US010838
                                                                                                                   15-MAY-2002 (first entry)
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Weaver Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AVAL-) AVALON PHARM.
                                                                                                                                                                                                                                                                                                                                                              WO200194629-A2
                                                                                                                                                                                                                                                                                                                      Homo sapiens
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Soppet DR,
                                                                            ABL65935;
                                                                                                                                                                                                                                                                            gene; ds.
         ABL 6593  
ABL 6593  
ABL 6593  
ABL 6593  
ABL 6593  
ABL 6594  
ABL 6594
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The invention relates to a method of diagnosing (I) the onset or progression of benign prostatic hyperplasia (BPH), or screening (II) for or identifying an agent that modulates the onset or progression of BPH.

The method is based on changes in gene expression in BPH tissue isolated from patients exhibiting different clinical states of prostate isolated to mormal prostate tissue. (I) comprises of prostate cells. (II) comprises of the expression levels of one or more genes in prostate cells from the subject that are differentially regulated compared to normal prostate cells. (II) comprises preparing a first gene expression profile of BPH cells or BPH-like cell population, exposing the cells to the supersing the first and second gene expression profile of BPH cales are useful to mose to repression profile of the agent exposed cells, and comparing the first and second gene expression profile. (II) is useful for diagnosing the onese to progression of BPH. The methods are useful to present information identifying the expression of genes given in the specification in the tissue or cells, by comparing the expression level of expression level in the specification in the tissue or cells to the level of expression level in the database, and displaying the expression levels of a Least one gene in the database, and displaying the prostatic cancer. ABR64106-ABR64106 represent human benign prostatic progression compared to the prostate cancer. ABR64106-ABR64106 represent human benign prostatic
                                                                                                                                                                      Identifying drugs for and diagnosing benign prostatic hyperplasia, by detecting expression levels of one or more genes in prostate cells from patient that are differentially regulated compared to normal prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP; 190 A; 164 C; 156 G; 180 T; 0 U; 7 Other;
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61.00
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                     (GENE-) GENE LOGIC INC. (NISB ) JAPAN TOBACCO INC.
                                                                                      Kulkarni P,
                                                                                                                              WPI; 2002-257476/30.
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158
                                                                                                                                                                                                 63 AAATACGAGAACGGGTACATTCACCCGGTCAACCTGACGTGGCCCTTTATGGTGGCCGGG 122
                                                                                                                                  62
                                                                                               119 AspThrLeuArgLeuAlaSerSerTyrIleAlaHisLeuArgGlnIleLeuAlaAsnAsp
                                                                                                                                                                                                                                                      AAACCCGAGAGTGACCTGAAAGAAGTGGTGGCGCGGGGCCGCTTATGTGGAACCCGCG
                                                                                                                                3 GACACGCTCAGGCTCCAGCTACATCGCCCACTTGAGGCAGATCCTGGCTAACGAC
                                                                                                                                                                  139 LysTyrGluAsnGlyTyrIleHisProValAsnLeuThrTrpProPheMetValAlaGly
                                                                                                                                                                                                                                 LysProGluSerAspLeuLysGluValValThrAlaSerArgLeuCysGlyThrThrAla
                                                               US-09-701-674A-23 (1-179) x ABK64784 (1-697)
                                                                                                                                                                                                                                                                                                                                                                                                   ABQ55427 standard; cDNA; 632 BP.
Best Local Similarity:
Query Match:
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Length: Matches:

Alignment Scores: Pred. No.: Score:

(first entry)

22-AUG-2002

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The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNAs encoding them (ABD54131-ABD55305), and also encompasses polypeptides 90% identical and polymucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigens to recombinant vectors and host cells comprising human ovarian antigens of ovarian antigens of ovarian antigens of ovarian antigens of ovarian or breast cancer and treating, prognosing or preventing various ovary and/or breast cancer, and casorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast corigin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation, collocated disorders (e.g., chlamydia, HV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, cophoritis and cisorders, inflammatory conditions (e.g., mastitis, cophoritis and vaginitis), immune disorders (e.g., congenital and acquired thouse conformations, autoimmune ophoritis, systems isorders, neurological disorders, gastrointestinal disorders. blood-related disorders, neurological disorders, gastrointestinal disorders. Compounds which modulate ovarian antigen expression or activity. The polymucleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polymucleotides may be used as food additives or to prepare antibodies classful in disease diagnosis, drug targeting and phenotyphng. The present sequence represents cDNA encoding a human ovarian antigen of the printed specification, but was obtained in electronic format directly from the printed specification, but was obtained in electronic format directly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ovarian
                                                              Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antibidammatory; gynaecological; reproductive; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful in the prevention, treatment and diagnosis of cancer (e.g. ovcancer), immune disorders, cardiovascular disorders and neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated nucleic acid molecules encoding novel ovarian polypeptides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 632 BP; 145 A; 176 C; 201 G; 93 T; 0 U; 17 Other;
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                    ovarian antigen HNOJ185 cDNA, SEQ ID NO:1307.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 1307; 2922pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JUN-2001; 2001WO-US018569.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-JUN-2000; 2000US-0209467P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-147878/19.
P-PSDB; ABP42350.
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                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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The invention relates to a combination which, comprises a number of polynucleotide probes comprising a sequence selected from one of the 1490 sequences mentioned in the specification. The combination is useful as an array element in a microarray for monitoring the expression of a number of target polynucleotides. The microarray is particularly useful in the diagnosts and immunopathology and neuropathology. The microarray is useful in diagnostics and treatment regimens, drug discovery and development, toxicological and carcinogenicity studies, forensics and pharmacogenomics. The microarray is also useful for monitoring progression of diseases and for developing sophisticated profiles for the effects of currently available therapeutic drugs. The combination is also useful for purifying a subpopulation of mRNAs, cDNAs array can detect changes in research and diagnostic applications. The array can detect changes in expression in a large number of genes coding for different signaling pathway populations which can be used to diagnose for different signaling pathway populations and leukaemia, immunopathies e.g. Alzheimer's disease in manual assemble e.g. Alzheimer's disease and parkinson's disease to expresents a polynucleotide
                                                                                                                                                                                                                                                                                                              82 AAAATGGATTCGAACAAGGAATTTGTGACTTCCAACGAGGAGCACCGAGGAGGCTCCAAC 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                   142 TGCGAGAATGGGTCTCCCCAGAAGGGCCGGGNGGCCTGGGCAAGAGGGAAGAGGCGCCC 201
                                                                                                                                                                                                                                                                                                                                                                                    63
                                                                                                                                                                                                                                               24 LysMetAspSerAsnLysGluPheValThrSerAsnGluSerThrGluGluSerSerAsn 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chicken; probe; ss; array element; Parkinson's disease;
signalling pathway population; cancer; adenocarcinoma; leukaemia;
immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
                                                                                                                                                                                                                                                                                                                                                                                    44 CysGluAsnGlySerProGlnLysGlyArgGlyGlyLeuGlyLysArgArgLysAlaPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Combination of polynucleotide probes, useful as array elements in a microarray for monitoring the expression of a number of target
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chicken signalling pathway polynucleotide probe SEQ ID NO 1028.
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Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 ThrLysLysSerProLeuSerGlyVal
                                                                                                                                                                             US-09-701-674A-23 (1-179) x ABQ55427
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polynucleotides.
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The invention relates to a composition of polynucleotide probes comprising first polynucleotide probes comprising at least a portion of a gene encoding a receptor-like polypeptide, second polynucleotide probes comprising at least a portion of a gene encoding a transducing polypeptide and third polynucleotide probes comprising at least a portion of a gene encoding a transducing of a gene encoding an effector-like polypeptide. The probes of the composition are useful as array elements in a microarray for monitoring
                                                                                                                                                                                                                                                                                                                                                  90 GCCCGCATGCGAGTGCTGAGCAAGGCCTTCTCCAGACTCAAGACCACCAGCCTGGGCTGGGTG 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; probe; ss; receptor-like polypeptide; transducing polypeptide; effector-like polypeptide; cancer; immunopathology; neuropathology; drug development; toxicology; carcinogenicity; signalling pathway polypeptide; adrenal gland; bladder; bone; signalling pathway polypeptide; adrenal gland; bladder; bone; bone marrow; brain, breast; cervix; tumnours; immunopathology; diabetes; pancreatitis; osteoporosis; ulcerative colitis; neuropathology; dementia; amnesia; epilepsy; Alzheimer's disease; depression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genomic
probe of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                                      90 AlaArgMetArgValLeuSerLysAlaPheSerArgLeuLysThrThrLeuProTrpVal
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                                                                                                                                                                                                                                                                                                                                                                                                    110 ProProAspThrLysLeuSerLysLeuAspThrLeuArgLeuAlaSer 125
                                                                                                                                                                                                                                                                                                                                                                                                                          150 CCCCCCGACACCAAGCTCTCCAAGCTGGACACGCTCAGGCTGGCGTCC 197
                                                                                            Sequence 240 BP; 55 A; 83 C; 72 G; 27 T; 0 U; 3 Other;
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human polynucleotide probe #1028.
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the expression of target polynucleotides. The microarray is useful in the diagnosis and treatment of cancer, an immunopathology or a neuropathology. It can also be used for drug discovery and development, toxicological and carcinogenicity studies, forensics or pharmacogenomics. Microarrays can also be used for monitoring the progression of diseases that may be associated with the altered expression of diseases that may be associated with the altered expression of diseases to polypeptides. The composition can also be used to purify a subpopulation of finds. Oppopulation of finds. Oppopulation of finds, or genomic fragments in a sample. The expression profile is also useful for the diagnosis and treatment of cancer, e.g. cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast or cervix, on immunopathology, e.g. Alzheimer's disease or depression. This sequence represents a ulcerative probe of the invention. Note: The sequence data for this patent did not form part of the printed specification but was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ss; sequencing by hybridisation; SBH; expressed sequence tag; BST; mapping; biodiversity; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90 AlaArgMetArgValLeuSerLysAlaPheSerArgLeuLysThrThrLeuProTrpVal
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STACHE-CRAIN B.
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(LABA/) LABAT I.
(STAC/) STACHE-CRAIN E
(DICK/) DICKSON M C.
(JONE/) JONES L W.
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The invention relates to an isolated polynucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SBH (Sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (BST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, or chromosome and gene mapping, in the recombinant production of protein, or in generating antibodies by the purified polypeptide is useful for generating antibodies specific for it. The present sequence is useful did not form part of the printed specification, but was for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Musculin; basic helix-loop-helix; bHLH; transcription factor; myogenesis; screening; myogenic disease; abberation; muscle development; cytostatic; gene therapy; diagnostic agent; muscular dystrophy; myopathy; neuromuscular; skeletomuscular; myogenic cancer; human; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        152 TrpProPheMetValAlaGlyLysProGluSerAspLeuLysGluValValThrAlaSer
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/note= "Lacks Alanine-Threonine myogenic recognition
mapping, in the recombinant production of protein, or in generating antisense DNA or RNA.
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 493 BP; 121 A; 136 C; 121 G; 112 T; 0 U; 3 Other;
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880000
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                                                    Claim 1; SEQ ID NO 11181; 44pp; English
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98AU-00004955

30-JUL-1998;

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New regulatory protein useful for gene therapy of myogenic cancer and for detecting aberrations in muscle development in myogenic disease, comprises protein associated with genes involved in myogenesis.
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                                                                                                                                                                                                     The present cDNA sequence encodes human musculin bHLH (basic helix-loophelix) protein, which is a transcription factor associated with genes from lim genesis. Musculin gene can be used in genetic screening for myogenic disease conditions, for detecting abberations in muscle development and in gene therapy. Anti-musculin natioodies can be used as therapputic or diagnostic agents. Musculin has eyeotatic activity and can be used to treat myogenic disease conditions like myopathies, muscular dystrophies, neuromuscular and skeletomuscular disorders and
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/note= "Lacks Alanine-Threonine myogenic recognition
motif"
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murine musculin bHLH protein encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (1-1716)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 3; Page 38-40; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-701-674A-23 (1-179) x AAZ50465
                                                     Harvey RP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAZ50464 standard; cDNA; 1718
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                                                     Begley CG,
                                                                                  WPI; 2000-195290/17
                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
                                                                                                 P-PSDB; AAY44922.
                                                                                                                                                                                                                                                                                                                             myogenic cancer
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                                                     Robb L,
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DB:
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for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, ss; differential expression; foam cell; LPS; lipopolysaccharide; cardiovascular disease; atherosclerosis.
                                                                                                                                                      New regulatory protein useful for gene therapy of myogenic cancer and detecting aberrations in muscle development in myogenic disease, comprises protein associated with genes involved in myogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106 LeuProTrpValProProAspThrLysLeuSerLysLeuAspThrLeuArgLeuAlaSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            603 CTGCCCTGGGTGCCGCCGACACCTAGCAACTTCCAAACTGGACACGCTGGGCCTGGCTTCC
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1718 BP; 356 A; 477 C; 520 G; 365 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human cDNA differentially expressed in foam cells #97.
                                                                                                                                                                                                                                                                                                                                                                                                                             1718
28
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Mismatches:
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                                                        (HALL-) HALL INST MEDICAL RES WALTER & ELIZA
                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Porter JG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             663 AGCTACATCGCGCACCTGCGCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ВP
                                                                                    Harvey RP
                                                                                                                                                                                                                 Claim 3; Fig 1A; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADE25693 standard; cDNA; 2177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-SEP-2002; 2002US-00247671
99WO-AU000623
                            98AU-00004955
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                                                                                   Begley CG,
                                                                                                                WPI; 2000-195290/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity:
cal Similarity:
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                                                                                                                                                                                                                                                                                                                                                               myogenic cancer
   30-JUL-1999;
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                              30-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
Pred. No.:
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                                                                                   Robb L,
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Best Local S
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No.:
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Baughn MR;

Lu AMD,

Yue H, Azimzai Y,

Hillman JL, Au-Young JL;

Tang YT, Lal P, I Tran B, Shih LL,

28-JAN-2000; 2000WO-US002237

Homo sapiens. WO200044900-A2

03-AUG-2000.

99US-0117904P 99US-0117905P

29-JAN-1999; 29-JAN-1999; (INCY-) INCYTE PHARM INC

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RESULT 14
ADJ56314
The invention relates to a combination comprising several polymucleotides having any one of 127 sequences (S1) such as the sequence of human complements of standarding ages, human mRNA for KIAAO310 protest, leadworfines A4 hydrolase, human mRNA for KIAAO310 protest, leadworfines A4 hydrolase, human G1-142 protein mRNA, human K+ channel beat 2 subunit complements. The cDNAs are differentially expressed in LBS (lipopolyaaccharide)-treated foam cells. Also included are containing an extended or full length gene from a library of nucleic acid sequences, an expression vector containing the nucleic acids, a host cell containing the vector, a purified polypeptide appearing as ABE25750 and ABE25751, producing a protein by culturing the host cell, and a composition comprising a purified antibody that specifically binds to the proteins. The foam cell-expressed nucleic acids are useful for a high throughput detection of differential expression of one or more polymucleotides in a sample. The sample is from a subject with a theorem comparison with a standard defines early, mid or late for high throughput screening of a library of molecules or compounds to identify a ligand which binds a polymucleotide. The library is chosen from DNA molecules, peptides, proteins and RNA molecules. The protein is useful for a high throughput screening of library of molecules or compounds to electin, for purifying a ligand from a sample for making a antibody. The foam cell-expressed mucleic acids are useful for cell-expressed mucleic acids are useful for compounds to identify at least one ligand which specifically binds a proteins are sample for making a antibody. The foam cell-expressed mucleic acids are useful for cell-expressed mucleic acids are useful for cell-expressed mucleic acids are useful for man part of a mucleic acids are useful for man expressed and the protein for cell-expressed mucleic acids are useful for man expressed and the protein are useful for man expressed and the protein are negative forms and the protein and the prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  foam cell-expressed nucleic acids are useful for diagnosing cardiovascular disorder. The foam cell-expressed nucleic acids are useful as elements on a microarray which can be used for detecting related polynucleotide in a sample, diagnosing cardiovascular disease, atherosclerosis. The present sequence represents a cDNA whose expression is upregulated in LPS treated foam cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LeuProTrpValProProAspThrLysLeuSerLysLeuAspThrLeuArgLeuAlaSer 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       857 craccordádracocococacacraadorocaadorodacacacocrodacradoroda 916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human nucleic acid-binding protein; NuABP; agonist; antagonist; EST; expressed sequence tag; drug screening; recombinant expression; antibody; reproductive disorder; infertility; immunological disorder; neurological disorder; cell proliferative disorder; cancer; tumour; ss.
                                                                         Combination containing several polynucleotide that are differentially expressed in foam cells and complements of the polynucleotides, useful for diagnosing cardiovascular disease or atherosclerosis.
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                                                                                                                                                         Claim 1; SEQ ID NO 97; 37pp; English.
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                 2003-875398/81.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
                 WPI; 2003-875398,
P-PSDB; ADE25769
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Sequences AAA72382-A72416 represent CDNAs encoding novel human nucleic acid-binding proteins (NuABPS; AAB20997-B21051). These CDNAs were produced by extension from an appropriate EST (expressed sequence tag) using primers designed using the EST. The invention also relates to wind primers designed using the EST. The invention also relates to expression constructs, host cells and transgenic organisms comprising a nutibodies against the human NuABPS, and also to methods of screening antibodies against the human NuABPS, and also to methods of screening condulators of human NuABPS, and also to methods of screening condulators of human NuABPS, and their agonists are used to treat diseases associated with overexpression or underexpression of functional NuABPS. Human NuABP proteins and nucleotides, and NuABP agonists and antagonists can be used to disagnose, treat and prevent reproductive, immunological, neurological, compositions of the invention include infertility, and compositions of the menstrual cycle and disruptions of the menstrual cycle and disruptions of spermatogenesis. Immunological disorders that may be treated include spermatogenesis. Immunological disorders such as multiple sclerosis, neurodegenerative conditions such as Alzheimer's disease and Parkinson's disease, prion diseases such as Creutzfeldt-Jakob disease and mental disorders such as schizophremia. Cell proliferative disorders that may be treated include a wide variety of cancers, and also arteriosis, cirrhosis and psoriasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LeufroTrpValProProAspThrLysLeuSerLysLeuAspThrLeuArgLeuAlaSer 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       916
                                                                                           Novel nucleic acid binding proteins, used to identify agonists and antagonists of them, for the treatment of reproductive, immunological, neurological and cell proliferative disorders including cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2196 BP; 438 A; 691 C; 653 G; 414 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                         Claim 4; Page 176; 180pp; English.
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WPI; 2000-499332/44.
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Best Local Similarity:
                                   P-PSDB; AAB21043
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Pred. No.:
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DB:
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This invention relates to novel isolated cDNAs that are differentially expressed in MYCN activated cells. Specifically, it refers to polymucleotide sequences that exhibit differential expression patterns in cells activated by the transactivator MYCN, where MYCN is a protoconcern that is amplified in neuroblastoma cells and is common in small oncogene that is amplified in neuroblastoma cells and is common in small cell lung cancers. The present invention describes these CDNA molecules as useful for in hybridisation assays to detect expression of nucleic acids (or complementary nucleic acids) in a present in a given sample, as well as for screening assays by identifying molecules or compounds that specifically bind the CDNA as a ligand and modulate function or activity. Accordingly, these compositions exhibit cytostatic activity and can also be used for gene therapy purposes. This polymucleotide sequence is a CDNA that is differentially expressed in MYCN activated cells, given in an expension of the invention. NOTE: This sequence does not appear in the US Patent Office at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LeuProTrpValProProAspThrLysLeuSerLysLeuAspThrLeuArgLeuAlaSer 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CIGCCTGGGGTGCCCCCCGACACTAAGCTCTCCAAGCTGGACACGCTCCGGCTCGGCTTCC 916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New genes regulated by MYCN activation, useful in gene therapy, particularly for treating a subject with e.g. neuroblastoma or other cancers, or for diagnosing, staging or monitoring the treatment of the
                                                                                                    Human cDNA differentially expressed in MYCN activated cells SeqID 120
                                                                                                                                      human; differential expression; transactivator; proto-oncogene; neuroblastoma; small cell lung cancer; cytostatic; gene therapy; ss; MYCN activated cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2196 BP; 438 A; 691 C; 653 G; 414 T; 0 U; 0 Other;
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plon SE,
standard; cDNA; 2196 BP
                                                                                                                                                                                                                                                                                                                     25-FEB-2002; 2002US-00084817.
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(NUCH/) NUCHTERN J G.
(PLON/) PLON S E.
(SHOH/) SHOHET J M.
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                               Homo sapiens.
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The present invention relates to the isolation of human polynucleotide sequences that are differentially expressed during foam cell differentiation. The polynucleotide sequences of the invention or a composition comprising these polynucleotides are useful as a high throughput method for detecting altered expression of one or more polynucleotides in a sample. The polynucleotides can be used in the diagnosis of disorders associated with foam cell development such as atherosclerosis, cerebral stroke, and cardiovascular disorders such as coronary artery disease. The polynucleotide sequences can also be used as the primers and probes. The polynucleotide sequences can also be useful in gene therapy. AAS94746-AAS95021 represent the human polynucleotide sequences of the invention are also expressed during foam cell differentiation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Composition useful for diagnosis of conditions, disorders or diseases associated with atherosclerosis, comprises several polynucleotides that are differentially expressed in foam cell development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shiffman D, Somogyi R, Lawn R, Seilhamer JJ, Porter GJ, Mikita T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, foam cell differentiation, atherosclerosis, cerebral stroke, cardiovascular disorder, coronary artery disease, gene therapy, ds.
                                                                                                                                                                           Human DNA sequence #83 expressed during foam cell differentiation.
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Mismatches:
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917 AGTTACATCGCTCACCTGCGCCAG 940
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                                                                                AAS94828 standard; DNA; 2382
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Best Local Similarity:
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Pred. No.:
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DB:
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Search completed: December 17, 2004, 01:22:05 Job time : 461 secs

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December 16, 2004, 19:03:27 ; Search time 728 Seconds (without alignments) 9646.299 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/Pub. Pub. Pub. seq:*
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/ptodata/1/pubpna/US10 NEW PUB.seq.*
/ptodata/1/pubpna/US11 NEW PUB.seq.*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum DB seq length: 2000000000
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		% Ouery				
No.	Score	Match	Match Length DB	DB	ID	Description
П	581	45.7	697	. 6		Sequence 829, App
73	581	45.7	697	σ	US-09-954-456-1245	Sequence 1245, Ap
ო	581	45.7		10	US-09-960-706-1028	Sequence 1028, Ap
4	581	45.7		10	US-09-873-319-679	Sequence 679, App
2	525.6	41.3		16	US-10-264-049-1307	Sequence 1307, Ap
0	466.2	36.7		σ	US-09-954-456-881	Sequence 881, App
0	466.2	36.7		σ	US-09-954-456-1431	Sequence 1431, Ap
ω υ	466.2	36.7		10	US-09-960-706-17	Sequence 17, Appl
თ	466.2	36.7	471	10	US-09-873-319-10	Sequence 10, Appl
10	434.2	34.1		10	US-09-918-995-11181	œ
11	297.2	23.4		10	US-09-918-995-9069	Sequence 9069, Ap
12	213	16.7		16	US-10-305-720-1028	Sequence 1028, Ap

97,	Sequence 120, App	201	83,	365	50	9 12	Sequence 22740, A	ŏ	ŏ	Ŋ	Sequence 22, Appl	à	a	Sequence 1950, Ap	음	Sequence 86, Appl	Sequence 25, Appl	Sequence 106, App	Sequence 2433, Ap	Sequence 2017, Ap	Ψ	Sequence 22, Appl	23	Sequence 451, App	Sequence 6324, Ap	1.4	14	1.1	Sequence 17, Appl	Sequence 17, Appl	Sequence 73, Appl	Sequence 17, Appl
US-10-247-671-97	US-10-084-817-120	US-10-775-169-201	US-10-240-965-83	US-10-755-889-365	US-09-833-381-505	US-10-450-826-124	US-10-029-386-22740	US-09-771-357-106	US-10-059-579-106	US-10-004-717-22	US-10-860-373-22	US-10-860-724-22	US-09-954-531-982	US-10-062-674-1950	US-10-240-965-119	US-10-175-523-86	US-10-466-164-25	US-10-335-053-106	US-09-880-107-2433	US-10-087-192-2017	US-10-331-053-61	US-09-749-728B-22	US-09-778-844-23	US-10-087-192-451	US-10-674-124A-6324	US-10-044-090-251	US-09-918-995-22633	US-09-918-995-25117	US-09-799-462A-17	9-836-91	US-09-738-630-73	-12
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16.6	16.6	16.5	16.4	15.6	6.4	6.2	5.6	5.6	5.6	5.6	5.6	5.6	5.5	5.5	5. 5.	5.4	5.4	5.4	5.4	5.4					5.3	5,3	5.3	5.5	5.2	5.2	5.2	5.2
211.6	211.6	210	208.6	198	81.8	78.4	71.8	71.8	71.8	71	71	71	69.4	69.4	69.4	69	68.8	68.8	68.89	68.2	68.2	. 89	9.79	9.19	67.4	67.4	66.8	66.2	66.2	66.2	66.2	66.2
13	14	15	16	17	18	13	20	21	22	23	24	25	56	27	28	20	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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## ALIGNMENTS

US-09-954-456-829; Application US/09954456; Sequence 829, Application US/09954456; Parent No. US2002011507741
GANERAL INFORMATION:
I TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cancer TITLE OF INVENTION: Sets FILE REFERENCE: 68290-76
CURRENT APPLICATION WHERE: US/60/233,617
PRIOR FILING DATE: 2001-09-18
PRIOR APPLICATION WHERE: US/60/233,617
PRIOR APPLICATION WHERE: US/60/234,923
PRIOR APPLICATION WHERE: US/60/234,923
PRIOR APPLICATION WHERE: US/60/235,134
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-26
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PRIOR FILING DATE: 2000-09-27
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PRIOR APPLICATION WHERE: US/60/235,711
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PRIOR APPLICATION WHERE: US/60/235,711
PRIOR APPLICATION WHERE: US/60/235,711
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-

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1159 GACTITICACAGTCACATITIADAAGTAATTCACTTAAAGATATATATTTTTTTTTTCAAACAA 1218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 ACAAATACGAGAAACGGGTACATTCACCCGGTCAACCTGACGTGGCCCTTTATGGTGGCCG
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Best Local Similarity 95.1%; Pred. No. 4.4e-132;
Matches 621; Conservative 0; Mismatches 27;
PRIOR APPLICATION NUMBER: US/60/235,134
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-26
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; OTHER INFORMATION: n=a,t,g or
US-09-954-456-1245
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ORGANISM: Homo sapiens
FEATURE:
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Patent No. US20020115057A1
GENERAL INFORMATION:
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cancer TILE REFERENCE: 689290-76
CURRENT APPLICATION NUMBER: US/09/954,456
CURRENT APPLICATION NUMBER: US/60/233,617
PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR PILING DATE: 2000-09-18
PRIOR PILING DATE: 2000-09-18
PRIOR PILING DATE: 2000-09-20
PRIOR PILING DATE: 2000-09-20
PRIOR FILING DATE: 2000-09-25
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                                                                                                                                                                                                                          Length 697
                                                                                                                                                                                                                   Query Match
Best Local Similarity 95.1%; Pred. No. 4.4e-132;
Matches 621; Conservative 0; Mismatches 27; Indels
            ; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: n=a,t,g or
US-09-954-456-829
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y Generated introduction:

APPLICANT: Munder, William E.
APPLICANT: Munder, Prakash
APPLICANT: Malkarni, Prakash
APPLICANT: Getzenberg, Robert H.
APPLICANT: Getzenberg, Robert H.
APPLICANT: Getzenberg, Twao
APPLICANT: Mamamocto, Jun
TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic
TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic
TITLE OF INVENTION: John Prepalasi Using Gene Expression Profiles
FILE REPERBENCE: 44921-5029-US
CURRENT FILING DATE: 2001-66-05
EARLIER APPLICATION NUMBER: US 60/223,323
EARLIER PILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 755
SEQ ID NO 679
LENGTH: 697
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Pred. No: 4.4e-132;
0; Mismatches 27;
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                                                                                                                                      ; Sequence 679, Application US/09873319A; Publication No. US20030134324A1; GENERAL INFORMATION:
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Best Local Similarity 95.1%;
Matches 621; Conservative (
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; OTHER INFORMATION: n = a or
US-09-873-319-679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
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                                                                                                RESULT 4
US-09-873-319-679
1219
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                                               | Sequence 1028, Application US/09960706
| Publication No. US20030134280A1
| GENERAL INFORMATION: US20030134280A1
| GENERAL INFORMATION: US20030134280A1
| APPLICANT: Munger, William E.
| TITE OF INVENTION: Gene Expression Profiles
| TITE OF INVENTION: Gene Expression Profiles
| FILE REFERENCE: 44921-5029-01US
| CURRENT APPLICATION NUMBER: US/09/960,706
| CURRENT FILING DATE: 2000-09-24
| PRIOR FILING DATE: 2000-08-07
| PRIOR FILING DATE: 2001-06-05
| NUMBER OF SEQ ID NOS: 1124
| SOFTHARE PATENTIN VET. 2.1
| SEQ ID NO 1028
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                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
              RESULT 3
US-09-960-706-1028
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NAME/KEY: misc_feature
LOCATION: (623]..(623)
OTHER INFORMATION: n equals a,t,g, or c
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NAME/KEY: misc feature
LOCATION: (629)
. OTHER INFORMATION: n equals a,t,g, or c
US-10-264-049-1307
                                                                            NAME/KEY: misc feature
LOCATION: (537)..(537)
OTHER INFORMATION: n equals a,t,g, or
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                 LOCATION: (498)..(498)
OTHER INFORMATION: n equals a,t,g,
                                                                                                                                      FEATURE:
NAME/KEY: misc_feature
LOCATION: (546). (546)
OTHER INFORMATION: n equals a,t,g,
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LOCATION: (552)..(552)
OTHER INFORMATION: n equals a,t,g,
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AGGAGCCTATCAATGTATCTTTTGTACAATATGTTGTAAAAATGTAGAATCATAGGATAGCT 540
                                                                                  541 GACTTTGACAGTCACATTTATAAAGTAATTCACTTAAAAGTAATATTTTTCCAACA---
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US-10-264-049-1307

Sequence 1307, Application US/10264049

Publication No. US20040005579A1

GENERAL INFORMATION:

APPLICAMT: Birse et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REPERENCE: PAI391

CURRENT APPLICATION NUMBER: US/10/264,049

CURRENT PILING DATE: 2002-10-04

PRIOR FILING DATE: 2001-06-07

PRIOR FILING DATE: 2001-06-07

NUMBER OF SEQ ID NOS: 4360

SOFTWARE: Patentin Ver. 3.1

SEQ ID NO 1307

LENGTH: 632
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OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (174)...(174)
FEATURE:
NAME/KEY: misc feature
LOCATION: (231)...(231)
OTHER INFORMATION: n equals a,t,g, or c
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LOCATION: (467)..(467)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
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LOCATION: (263)...(263)
LOCATION: (263)...(263)
PEATURE:
NAME/KEY: misc_feature
LOCATION: (265)...(265)
OTHER INFORMATION: n equals a,t,g, 03
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LOCATION: (249)
OTHER INFORMATION: n equals a,t,g,
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MANG/KEY:
LOCATION: (331)..(331)
OTHER INFORMATION: n equals a,t,g,
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LOCATION: (280)..(280)
OTHER INFORMATION: n equals a,t,g,
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LOCATION: (433)...(433)
OTHER INFORMATION: n equals a,t,g,
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US-US-994-46-1431, Application US/09954456

| Bequence 1431, Application US/09954456
| Patent No. US20020115057A1
| GENERAL INFORMATION:
| APPLICANT: Young, Pend
| TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cancer TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cancer TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Days: US-00-109-18
| FILE REPERBNCE: 689290-76 | CURRENT FILING DATE: 2000-09-18 |
| PRIOR FILING DATE: 2000-09-18 |
| PRIOR FILING DATE: 2000-09-26 |
| PRIOR PLICATION NUMBER: US/60/235,637 |
| PRIOR FILING DATE: 2000-09-26 |
| PRIOR PLING DATE: 2000-09-26 |
| PRIOR FILING DATE: 2000-09-27 |
| PRIOR APPLICATION NUMBER: US/60/235,720 |
| PRIOR APPLICATION NUMBER: US/60/235,840 |
| PRIOR APPLICATION NUMBER: US/60/235,840 |
| PRIOR PLING DATE: 2000-09-27 |
| PRIOR APPLICATION NUMBER: US/60/235,840 |
| PRIOR PLING DATE: 2000-09-27 |
| PRIOR APPLICATION NUMBER: US/60/235,840 |
| PRIOR PLICATION NUMBER: US/60/235,840 |
| PRIOR PLICATION NUMBER: US/60/235,840 |
| PRIOR PLING DATE: 2000-09-27 |
| PRIOR PLING DATE: 2000-09-20 
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51 TITCAAACAAGTITIGCTACITITIGAAAATAAATCTITCTITATATIGCTA
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Pred. No. 5.2e-104;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin version 3.0
SEQ ID NO 1431
LENGTH: 471
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llarity 99.4%;
Conservative
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Best Local S
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                                                                            Sequence 881, Application US/09954456

Petent No. US20020110057A1

GENERAL INFORMATION:

JAPLICANT: YOUNG, Paul

JITLE OF INVENTION: Pacess for Identifying Anti-Cancer Therapeutic Agents Using Canc

JITLE OF INVENTION: Pacess for Identifying Anti-Cancer Therapeutic Agents Using Canc

JITLE OF INVENTION: Pacess for Identifying Anti-Cancer Therapeutic Agents Using Canc

JITLE OF INVENTION: Pacess for Identifying Anti-Cancer Therapeutic Agents USES TILE REPRENCE: 689290-76

CURRENT APPLICATION NUMBER: US/60/234,052

PRIOR FILING DATE: 2000-09-18

PRIOR FILING DATE: 2000-09-25

PRIOR APPLICATION NUMBER: US/60/235,134

PRIOR FILING DATE: 2000-09-25

PRIOR PAPILCATION NUMBER: US/60/235,111

PRIOR FILING DATE: 2000-09-26

PRIOR PAPILCATION NUMBER: US/60/235,111

PRIOR FILING DATE: 2000-09-26

PRIOR PAPILCATION NUMBER: US/60/235,111

PRIOR PAPILCATION NUMBER: US/60/235,111

PRIOR PAPILCATION NUMBER: US/60/235,720

PRIOR PELING DATE: 2000-09-27

PRIOR PELI
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Pred. No. 5.2e-104;
0; Mismatches 3;
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Best Local Similarity 99.4%;
Matches 468; Conservative
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CRGANISM: Homo sapiens
US-09-954-456-881
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us-09-701-674a-54.rnpb

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APPLICANT: Munger, William E.
APPLICANT: Kulkarni, Prakash
APPLICANT: Kulkarni, Prakash
APPLICANT: Getzenberg, Robert H.
APPLICANT: Waga, Iwao
APPLICANT: Vamamoto, Jun
TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic
TITLE OF INVENTION: Hyperplasia Using Gene Expression Profiles
FILE REFERENCE: 44921-5029-US
CURRENT PELING DATE: 2001-06-05
EARLIER APPLICATION NUMBER: US 60/223,323
BARLIER PILING DATE: 2000-08-07
SOFTWARE: PATENTION OF SEQ ID NOS: 755
SOFTWARE: PATENTION OF SEQ ID NOS: 755
SSOFTWARE: PATENTION OF SEQ ID NOS: 755
SSOFTWARE: PATENTION OF SEQ ID NOS: 755
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US-09-873-319-10
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Publication No. US20030073623A1
GENERAL INFORMATION:
APPLICANT: Hyeaq, Inc.
TITLE OF INVENTION: FROW VARIOUS CDNA LIBRARIES
FILLE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT APPLICATION NUMBER: US/09/235,076
FRIOR APPLICATION NUMBER: US/09/235,076
FRIOR FILING DATE: 1999-01-20
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Pred. No. 5.2e-104;
0; Mismatches 3;
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ORGANISM: Homo sapiens
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US-09-918-995-11181
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                                                                                                                                                                                                                                                           Publication No. US20030134280A1
| Publication No. US20030134280A1
| SENERAL INFORMATION: US20030134280A1
| GENERAL INFORMATION: US20030134280A1
| GENERAL INFORMATION: Udentifying Drugs for and Diagnosis of Benign Prostatic Hyperplas TITLE OF INVENTION: Gene Expression Profiles
| TITLE OF INVENTION: Gene Expression Profiles
| TITLE OF INVENTION: Gene Expression Profiles
| TITLE OF INVENTION: 2001-09-24
| CURRENT APPLICATION NUMBER: US/09/960,706
| PRIOR APPLICATION NUMBER: US/023,323
| PRIOR APPLICATION NUMBER: 09/23,323
| PRIOR FILING DATE: 2001-06-07
| PRIOR FILING DATE: 2001-06-05
| NUMBER OF SEQ ID NOS: 1124
| SOFTWARE: PatentIn Ver. 2.1
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111 TAGGATAGCTGACTTTGACAGTCACATTTATAAAGTAATTCACTTAAAGATATATTT
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                                                            1209 TITCAAACAAGIITIGCIACIITIGAAAATAAAATCIITIGITATATIGCIA 1259
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; CTHER INFORMATION: Genbank Accession No. US20030134280A1 AA028092
US-09-960-706-17
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                                                                                                                     3; Indels
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36.7%; Score 466.2; DB 10;
Best Local Similarity 99.4%; Pred. No. 5.2e-104;
Matches 468; Conservative 0; Mismatches 3; 1
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                          RESULT 8
US-09-960-706-17/c
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LENGTH: 471
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Sequence 10, Application US/09873319A Publication No. US20030134324A1

RESULT 9 US-09-873-319-10/c

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Sequence 1028, Application US/10305720
Publication No. US20040010136A1
Publication No. US20040010136A1
Publication No. US20040010136A1
APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression FILE OF INVENTION NUMBER: US/10/305,720
CURRENT FILING DATE: 2002-11-26
PRIOR PELLING DATE: 1998-01-30
NUMBER OF SEQ ID NOS: 1490
SOFTWARE: PERL PROGRAM
SOFTWARE: PERL PROGRAM
SOFTWARE: PERL PROGRAM
SOFTWARE: PERL PROGRAM
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                                           Length 482;
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16.7%; Score 213; DB 16; Length 240;
Best Local Similarity 97.9%; Pred. No. 5e-42;
Matches 235; Conservative 0; Mismatches 3; Indels
                                                                                                      Indels
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NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20040010136A1 954226
                                           10;
                                    Score 297.2; DB 10;
Pred. No. 1.6e-62;
0; Mismatches 9;
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| OTHER INFORMATION: a, t, c, g, or other
US-10-305-720-1028
                                        Query Match
23.4%;
Best Local Similarity 97.1%;
Matches 302; Conservative
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ORGANISM: Homo sapiens
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NAME/KEY: unsure
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APPLICANT HYSEG, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
CURRENT APPLICATION NUMBER: US/09/215,076
CURRENT FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FESUSEQ for Windows Version 3.0
SEQ ID NO 9069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 34.1%; Score 434.2; DB 10; Best Local Similarity 99.3%; Pred. No. 3.8e-96; Matches 436; Conservative 0; Mismatches 3;
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 11181
LENGTH: 493
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Publication No. US20030073623A1
GENERAL INFORMATION:
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                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
PEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(493)
OTHER INFORMATION: n = A,T,C or G
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US-09-918-995-9069
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APPLICANT: Mixita, Thomas
APPLICANT: Shiffman, Dov
APPLICANT: Shiffman, Dov
APPLICANT: Shiffman, Dov
TILLS TOTTEN Gordon, J.
TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS
FILE REPRENCE: PA-0050 US
CURRENT APPLICATION NUMBER: US/10/247,671
CURRENT FILING DATE: 2002-09-18
PRIOR APPLICATION NUMBER: 60/323,784
PRIOR PILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 186
SOFTWARE: PERL PROGram
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; OTHER INFORMATION: Incyte ID No. US20030194721A1 3282941CB1
US-10-247-671-97
                                                                                                                                                                                                                                ; Sequence 97, Application US/10247671; Publication No. US20030194721A1; GENERAL INFORMATION:
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                                                                                                                                                                     RESULT 13
US-10-247-671-97
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Sequence 120, Application US/10084817 Publication No. US20030119009A1 GENERAL INFORMATION:

RESULT 14 US-10-084-817-120

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APPLICANT: Wyeth
APPLICANT: Burczynski, Michael
APPLICANT: Twine, Natalie
APPLICANT: Twine, Natalie
APPLICANT: Trepicchio, William
TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo-
FILE REFERENCE: AMIONO (031896-013000)
FURRENT APPLICATION NUMBER: US/10/775,169
CURRENT FILING DATE: 2004-02-11
NUMBER OF SEQ ID NOS: 5278
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16.6%; Score 211.6; DB 15; Length 2196;
Best Local Similarity 68.5%; Pred. No. 3.6e-41;
Matches 292; Conservative 0; Mismatches 134; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
; NAME/KER:
; OTHER INTORMATION: Incyte ID No. US20030119009A1 3282941CB1
US-10-084-817-120
APPLICANT: Jed G. Nuchtern
APPLICANT: Aharon E. Plon
APPLICANT: Abaron M. Shohet
TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION
TITLE OF INVENTION WINDER: US/10/084,817
CURRENT FILING DATE: 2002-02-25
FRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 365
SOFTWARE: PELL PROGRAM
SEQ ID NO 120
IENGTH: 2196
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Publication No. US20040175743A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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Best Local Similarity
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                                                                                                                                Score 210; DB 17; Length 1716;
Pred. No. 7.8e-41;
0; Mismatches 135; Indels 0
; SOFTWARE: Patentin version 3.2
; SEO ID NO 201
; LENGTH: 1716
; TYPE: DNA
; ORGANISM: Homo sapiens ...
US-10-775-169-201
                                                                                                                                Query Match
Best Local Similarity 68.3%;
Matches 291; Conservative
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Sequence 6600, Ap
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Sequence 16285, A
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Sequence 1244, App
Sequence 12100, A
Sequence 2211, Ap
Sequence 12072, A
Sequence 12072, A
Sequence 5677, Ap
Sequence 12072, A
Sequence 5677, Ap
Sequence 15919, A
Sequence 16399, A
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US-09-016-434-1028
i Sequence 1028 Application US/09016434
j Patent No. 6500938
j GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffley J. Sellhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
OVERSEPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STRET: 3174 PORTER DRIVE
COUTRY: USA
STRET: JA104
CCOMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER: Mord Perfect 6.1 for Windows/MS-DOS 6.2
SUBTRING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
FILING DATE: HERBWITH
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                   US-09-313-294A-51675

US-09-702-705-735

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US-09-618-1244-735

US-09-68-1244-735

US-09-252-991A-13449

US-09-252-991A-13449

US-09-252-991A-16285

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US-09-618-976-14307

US-09-270-767-2659

US-09-270-767-2659

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ATTORNEY AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-01
TELEPHONE: (650) 855-0555
                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                       December 17, 2004, 01:07:28 ; Search time 88 Seconds (without alignments) 1445.809 Million cell updates/sec
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6: /CGT2_6/ptodata/l/ina/PCTUS_COMB.seq:*
                            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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; Patent No. 6703491
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-18376
                                                                                          ) TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-3094
 CURRENT FILING DATE: 1999-03-17
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                 NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3094
LENGTH: 276
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Best Local Similarity:
Query Match:
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Query Match:
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US-09-489-039A-1390/c

is Sequence 1390, Application US/09489039A

patent No. 6610836

GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: NUMBER: US/09/489,039A

CURRENT APPLICATION NUMBER: US 60/117,747

PRIOR PEPLICATION NUMBER: US 60/117,747

PRIOR SEPLIATION APPLICATION NUMBER: US 60/117,747

NUMBER OF SEQ ID NOS: 14342

LENGTH: 2610

LENGTH: 2610
                                                                                                                                                                                                                                                                                                                                                                                                         90 AlaArgMetArgValLeuSerLysAlaPheSerArgLeuLysThrThrLeuProTrpVal 109
                                                                                                                                                                                                                                                                                                                                                                                                                                          90 GCCCGCATGCGAGTGCTGAGCCAAGGCCTTCTCCAGACTCAAGACCACCCTGCCCTGGGTG 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Homburger et al. TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094 CURRENT APPLICATION NUMBER: US/09/270,767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              110 ProProAspThrLysLeuSerLysLeuAspThrLeuArgLeuAlaSer 125
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3094, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 103
SEQUENCE CHARACTERISTICS:
LENGTH: 240 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
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CLONE: 954226
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Best Local Similarity:
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Best Local Similarity:
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US-09-270-767-3094/c
                                                                                                                                                                                    US-09-016-434-1028
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APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 18976
LENGTH: 276
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APPLICANT: Ford, Donna M.
APPLICANT: Lewis, Marcia E.
APPLICANT: Lewis, Marcia E.
APPLICANT: Schlegel, Yober
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-701-674A-23 (1-179) x US-09-270-767-18376 (1-276)
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Conservative:
Mismatches:
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1: Griffith Hack & Co
Level 8, 168 Walker Street
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Best Local Similarity:
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US-08-793-824-1
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US-09-489-039A-5852/c
US-09-489-039A-5852/c
| Sequence 5852, Application US/09489039A
| Patent No. 6610836
| GENERAL INFORMATION:
| APPLICANT: Gary Breton et. al
| TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
| TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
| FILE REFERENCE: 2709.2004001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10281
LENGTH: 1013
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Matches:
Conservative:
Mismatches:
Indels:
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TITLE OF INVENTION: PRODUCTS
FILE REPERENCE: CD-257 (US)
CURRENT APPLICATION NUMBER: US/09/328,111
CURRENT FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: US 60/088,801
EARLIER APPLICATION NUMBER: US 60/088,801
SOFTWARE: FASTERO FOR SEQ ID NOS: 850
SOFTWARE: FASTERO FOR Windows Version 3.0
SEQ ID NO 493
LENGTH: 633
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Patent No. 6703491
GENERAL INFORMATION:
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ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                NAME/KEY: misc feature
LOCATION: (1).T.(633)
OTHER INFORMATION: n = A,T,C or
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FEATURE:
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Best Local Similarity:
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Pred. No.:
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US-09-489-039A-5698
US-09-489-039A-5698
US-09-489-039A-5698
Sequence 5698, Application US/09489039A
Fatent No. 6610836
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUMBER: US/09/489,039A
FILE REPERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT PELING DATE: 1999-01.27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
NUMBER OF SEQ ID NOS: 14342
LENGTH: 2595
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Increase Stored Carbohydrates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-701-674A-23 (1-179) x US-09-489-039A-5852 (1-1893)
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
CURRENT APPLICATION NUMBER: US/09/489,039A CURRENT FILING DEE: 2000-01-27 PRIOR APPLICATION NUMBER: US 60/117,747 PRIOR FILING DATE: 1999-01-29 NUMBER OF SEQ ID NOS: 14342 LENGTH: 1893
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APPLICANT: Simpson, Christine Lynn
APPLICANT: Giffard, Philip Morrison
APPLICANT: Jacques, Nicholas Anthony
TITLE OF INVENTION: Genetic Manipulatic
TITLE OF INVENTION: Increase Stored Can
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1433 CGGTTGGCGTCGTCATACATCGCC 1410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 ArgleuAlaSerSerTyrileAla 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 ArgleuAlaSerSerTyrIleAla 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Klebsiella pneumoniae US-09-489-039A-5698
                                                                                                                                                                                      , TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-5852
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RESULT 10
US-09-443-199C-469/C
is Sequence 469. Application US/09443199C
is Patent No. 6674464
is GENERAL INFORMATION:
is APPLICANT: Shinkers, Richard A.
is APPLICANT: Laach, Martin
if TITLE OF INVENTION: Nucleic Acids Containing Single Nucleotide
if TITLE OF INVENTION: Polymorphisms and Methods of Use Thereof
if TITLE OF INVENTION: Polymorphisms and Methods of Use Thereof
if TITLE OF INVENTION: NUMBER: US/09/443,199C
is CURRENT APPLICATION NUMBER: 00/109,024
is PRIOR PILING DATE: 1998-11-17
is NUMBER OF SEQ ID NOS: 1272
is SOFTWARE: Curaden Patent Formatter Version 0.9
is SEQ ID NO 469
is IRNGTH: 51
if TYPE: DRA
if MARCHISM: Home sapiens
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NAME/KEY: misc_feature
LOCATION: (26)_...(0)
OTHER INFORMATION: 1 of 2 allelic variants (470 is other entry)
NAME/KEY: misc_feature
LOCATION: (0)...(0)
                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SEM PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,824
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           165 LysGluValValThrAlaSerArg 172
                                                                                                                                                                                                                                                        PAIGNAIPICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PM7643
FILING DATE: 24-AUG-1994
TELECOMMUNICATION INFORMATION:
TELEFAN: 61 2 957 5944
                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 0.7
TELEX: 26547
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4853 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
No. 5981838th Sydney
New South Wales
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
ANTI-SPANO
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Query Match:
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Sequence 91, Application US/09237712

Patent No. 6180391

GENERAL INFORMATION:

APPLICANT: BROWN, WILLIAM C.

TITLE OF INVENTION: HIGHLY EFFICIENT CONTROLLED EXPRESSION OF EXOGENOUS

TITLE OF INVENTION: GENES IN E. COLI

TITLE OF INVENTION: GENES IN E. COLI

FILE REFERENCE: A-518

CURRENT APPLICATION NUMBER: US/09/237,712

CURRENT FILING DATE: 1999-01-26

EARLIER FILING DATE: 1998-01-28

NUMBER OF SEQ ID NOS: 98

SOFTWARE: PATENTING DATE: 200

SSOTUM RES: PATENTING VET: 2.0

LENGTH: 88
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US-09-513-999C-14487/C
Sequence 14487, Application US/09513999C
Factor No. (783961)
GENERAL INFORMATION:
FAPPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
FAPPLICANT: Duclert, A.
FILE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 200.0-02-24
CURRENT FILING DATE: 1999-00-26
FILE REPERENCE: 59.US2.8681
CURRENT FILING DATE: 1999-00-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 14487
LENGTH: 151
TYPE: DNA
ORGANISM: Homo sapiens
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Mismatches:
Indels:
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; OTHER INFORMATION: Accession number cg32177197
US-09-443-199C-469
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                                                                                                                                                                                                                                                                   169 ThralaSerArgLeuCysGly 175
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3.91%
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Percent Similarity: 100.00%
Dest Local Similarity: 100.00%
Query Match:
3.91%
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, ORGANISM: oligonucleotide
US-09-237-712-91
                                                                                                                        Percent Similarity:
Best Local Similarity:
                                                              Alignment Scores:
Pred. No.:
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OTHER INFORMATION: Incyte ID No. 6476212 700349712H1
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Matches:
Conservative:
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Indels:
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                               NAME/KEY: unsure
LOCATION: 81
OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-5167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 735, Application US/09702705; Patent No. 6504010; GENERAL INFORMATION:
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Bangur, Chaitanya S.
Lodes, Michael A.
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; ORGANISM: Homo sapien
US-09-702-705-735
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US-09-313-294A-5167/C
US-09-313-294A-5167/C
Sequence 5167, Application US/09313294A
Fatent No. 6476212
GENERAL INFORMATION:
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Sherman, Bradley X.
TILLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR PILE REFERENCE: PL-0017 US
CURRENT PILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL PROGram
SEQ ID NO 5167
LENGTH: 176
LENGTH: 176
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| Sequence 20456, Application US/09513999C
| GENERAL INFORMATION:
| APPLICANT: Duclett, A. | PAICH REFERENCE: 59.02.REG | CURRENT APPLICATION NUMBER: US 60/122,487 | PRIOR FILING DATE: 199-02-26 | NUMBER OF SEQ ID NOS: 36681 | SOFTHARE: PAICHT PRICATION NUMBER: Duclett, pm | Control of the Applicant of the A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-701-674A-23 (1-179) x US-09-513-999C-20456 (1-158)
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Matches:
Conservative:
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Indels:
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Matches:
Conservative:
Mismatches:
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ORGANISM: Homo sapiens
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Best Local Similarity:
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      US-09-513-999C-14487
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APPLICANT: Panger, Gary
APPLICANT: Panger, Gary
APPLICANT: Carter, Darrick
APPLICANT: Reter, Marc
APPLICANT: Reter, Marc
APPLICANT: Reter, Marc
APPLICANT: Reter, Marc
APPLICANT: Pan, Lidyun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REPRENCE: 2.0121.478614
CURRENT APPLICATION NUMBER: US/09/702,705
CURRENT FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 1833
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 735
LENGTH: 216
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Matches:
Conservative:
Mismatches:
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Sequence 9069, Ap

Description

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APPLICAMT: Hypeq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REPRENCE: 2011-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT RILING DATE: 1999-01-20
PRIOR PILING DATE: 1999-01-20
NUMBER: OF SEQ ID NOS: 38054
SOFTWARE: PRESENCE for Windows Version 3.0
SEQ ID NO 9069
                                  0.05-918-995-9069
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0.05-99-910-1028
0.05-99-910-1028
0.05-99-910-201
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Publication No. US20030073623A1
GENERAL INFORMATION:
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119
110
110
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110
              DB
              Length
                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
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Match 1
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                                                                                                                                                  US-09-701-674A-23
179
1 MSTGSLSDVEDLQEVEMLEC......PBSDLKEVVTASRLCGTTAS
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1: /cgn2_6/ptodata/1/Pubpna/USO7_PUBCOMB.seq:*
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15: /cgn2_6/ptodata/1/Pubpna/USO0_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/Pubpna/USO0_PUBCOMB.seq:*
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         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                              protein - nucleic search, using frame_plus_p2n model
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Maximum DB seq length: 200000000
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Delop 6.0
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Perfect score:
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Sequence

SUMMARIES

Sequence 829, App Sequence 1245, App Sequence 1028, App Sequence 11028, App Sequence 11028, App Sequence 110, App Sequence 120, App Sequence 120, App Sequence 120, App Sequence 121, App Sequence 131, App Sequence 100, App Sequence 10043, App Sequence 10043, App Sequence 10043, App Sequence 10044, A Sequence 1134, A Sequence 11344, A Sequence 11234, A Sequence 11234,

158 122

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GENERAL INCOMENTION: Percess for Identifying Anti-Cancer Therapeutic Agents Using Cancer TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cancer TITLE OF INVENTION: Sets of FILE REPRENCE: 689290-76
FILE REPRENCE: 689290-76
CURRENT APPLICATION NUMBER: US/60/23,617
FRICK FILING DATE: 2000-09-18
FRICK FILING DATE: 2000-09-18
FRICK FILING DATE: 2000-09-26
FRICK FILING DATE: 2000-09-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 159 LysprogluSerAspLeuLysGluValValThrAlaSerArgLeuCysGlyThrThrAla 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 AspThrLeuArgLeuAlaSerSerTyrIleAlaHisLeuArgGlnIleLeuAlaAsnAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         139 LysTyrGluAsnGlyTyrIleHisProValAsnLeuThrTrpProPheMetValAlaGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 AATRACGAGAACGGGTACATTCACCCGGTCAACCTGACGTGGCCCTTTATGGTGGCCGGG
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Matches:
Conservative:
Mismatches:
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Patent No. US20020115057A1
GENERAL INFORMATION:
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CRGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: n=a,t,g or us.09-954-456-1245
          ; OTHER INFORMATION: n=a,t,g or
US-09-954-456-829
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APPLICANT: Young, Paul

TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc

TITLE OF INVENTION: Sets

CURRENT APPLICATION NUMBER: US/60/23,617

PRIOR APPLICATION NUMBER: US/60/234,923

PRIOR PLING DATE: 2000-09-25

PRIOR PLING DATE: 2000-09-25

PRIOR PLING DATE: 2000-09-25

PRIOR PLING DATE: 2000-09-26

PRIOR PLING DATE: 2000-09-26

PRIOR APPLICATION NUMBER: US/60/235,637

PRIOR APPLICATION NUMBER: US/60/235,637

PRIOR APPLICATION NUMBER: US/60/235,720

PRIOR PLING DATE: 2000-09-26

PRIOR PLING DATE: 2000-09-27

PRIOR PLING DATE: 2000-09-27

PRIOR PLING DATE: 2000-09-27

PRIOR PLING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: US/60/235,840

PRIOR PRIOR PLING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: US/60/235,840

PRIOR APPLICATION NUMBER: US/60/235,840

PRIOR PLING DATE: 2000-09-27

PRIOR PLING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: US/60/235,840

PRIOR PLING DATE: 2000-09-27

PRIOR PLING DATE: 2000-09-27
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Matches:
Conservative:
Mismatches:
Indels:
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; OTHER INFORMATION: n = A,T,C or US-09-918-995-9069
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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US-09-954-456-829
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APPLICANT: Munger, William E.
APPLICANT: Munger, William E.
APPLICANT: Multiam E.
APPLICANT: Manger, William E.
APPLICANT: Getzenberg, Robert H.
APPLICANT: Getzenberg, Robert H.
APPLICANT: Manger, Iwao
APPLICANT: Multiple Manger, Iwao
APPLICANT: Multiple APPLICATION NUMBER: US 60/223,323
APPLICANT: Multiple APPLICATION NUMBER: US 60/223,323
APPLICANT: Multiple APPLICANT: Mult
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Publication No. US20040005579A1
GENERAL INFORMATION:
APPLICANT: Birse et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERENCE: PA133P1
CURRENT APPLICATION UNMBER: US/10/264,049
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/18569
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NAME/KEY: unsure
LOCATION: (1)..(697)
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US-09-873-319-679
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Query Match:
DB:
                                    Ser 179
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US-10-264-049-1307
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US-09-873-319-679
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Sequence 1028, Application US/09960706

Publication No. US2030134280A1

Sequence 1028, Application US/09960706

Publication No. US2030134280A1

APPLICANT: Munger, William E.

TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperplas

TITLE OF INVENTION: Gene Expression Profiles

TITLE OF INVENTION: Gene Expression Profiles

CURRENT APPLICATION NUMBER: US/09/960,706

CURRENT APPLICATION NUMBER: 60/223,323

PRIOR FILING DATE: 2001-06-05

PRIOR PAPLICATION NUMBER: 60/223,323

PRIOR PAPLICATION NUMBER: 09/873,319

PRIOR PLING DATE: 2001-06-05

NUMBER OF SEQ ID NOS: 1124

SOFTWARE: PATENTI Ver. 2.1.

SEQ ID NO 1028

TENGTH: 697
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LOCATION: (1). (697)
OTHER INFORMATION: n = a or
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ORGANISM: Homo sapiens
FEATURE:
          Percent Similarity:
Best Local Similarity:
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PRIOR FILING DATE: 2001-06-07
PRIOR PEDLICATION NUMBER: US 60/209,467.
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 4360
SEG ID NOS: 4360
SEQ ID NO 1307
LENGTH: 632
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LOCATION: (629)..(629)
OTHER INFORMATION: n equals a,t,g, or
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NAME/KEY: misc feature
LOCATION: (1747..(174)
OTHER INFORMATION: n equals a,t,g, or
FEATURE:
NAME/KEY: misc feature
LOCATION: (2317..(231)
OTHER INFORMATION: n equals a,t,g, or
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LOCATION: (78)...(79)
OTHER INFORMATION: n equals a,t,g,
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MANDKKEY: misc_feature
LOCATION: (249). (249)
OTHER INFORMATION: n equals a,t,g,
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NAME/KEY: misc_feature
LOCATION: (265)..(265)
OTHER INFORMATION: n equals a,t,g,
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COCATION: (280)
OTHER INFORMATION: n equals a,t,g,
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LOCATION: (433)
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NAME/KEY: misc_feature
LOCATION: (467)..(467)
OTHER INFORMATION: n equals a,t,g,
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LOCATION: (498)..(498)
OTHER INFORMATION: n equals a,t,g,
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LOCATION: (537)..(537)
OTHER INFORMATION: n equals a,t,g,
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MAMS/KEY: misc_feature
LOCATION: (552). (552)
OTHER INFORMATION: n equals a,t,9,
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LOCATION: (331)...(331)
OTHER INFORMATION: n equals a,t,g,
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LOCATION: (546)..(546)
OTHER INFORMATION: n equals a,t,g,
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THER INFORMATION: n equals a,t,g,
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LOCATION: (263)...(263)
OTHER INFORMATION: n equals
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NAME/KEY: misc_feature
'~~~rown: (623)..(623)
                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                      TYPE: DNA
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APPLICANT: AL-Young, Janice K.; Seilhamer, Jeffrey J.
APPLICANT: AL-Young, Janice K.; Seilhamer, Jeffrey J.
TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression FILE REPRENCE: PA-0002-1 CON
CURRENT APPLICATION NUMBER: US/10/305,720
CURRENT APPLICATION NUMBER: 09/016,434
PRIOR FILING DATE: 1998-01-30
NUMBER OF SEQ ID NOS: 1490
SOFTWARE: PERL PROGram
SEQ ID NO 1028
LENGTH: 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90 AlaArgMetArgValLeuSerLysAlaPheSerArgLeuLysThrThrLeuProTrpVal 109
                                                                                                                                                                                                                       82 AAAATGGATTCGAACAAGGAATTTGTGACTTCCAACGAGAGCACCGAGGAGAGCTCCAAC 141
                                                                                                                                                                                                                                                                                                142 TGCGAGAATGGGTCTCCCCAGAAGGCCGCGGGNGGCCTGGGCAAGAGAGGAGGCCC 201
                                                                                                                                                                                                                                                                     63
                                                                                                                                                                                                                                                                     44 CysgluhsnglySerProglnLysglyArgGlyGlyLeuglyLysArgLysAlaPro
                                                                                                                                                                                               24 LysMetAspSerAsnLysGluPheValThrSerAsnGluSerThrGluGluSerSerAsn
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OTHER INFORMATION: Incyte ID No. US20040010136A1 954226
FEATURE:
NAME/KEY: unsure
LOCATION: (1) ... (240)
LOCATION: (1) ... (240)
US-10-305-720-1028
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Matches:
Conservative:
Mismatches:
Indels:
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Mismatches:
Indels:
                                               Length:
Matches:
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5.09-918-995-11181
5.8equence 11181, Application US/09918995
publication No. US20030073623A1
                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-305-720-1028
Sequence 1028, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
PEATURE:
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Best Local Similarity:
US-10-264-049-1307
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Sequence 365, Application US/10755889
Publication No. US20040171823A1
GENERAL INFORMATION
APPLICANT: Bristol-Myers Squibb Company
ITILE OF INVENTION: PATHWAY
FILE REFERENCE: D0284 NP
CURRENT FILING DATE: 2004-01-13
PRIOR APPLICATION NUMBER: U.S. 60/440,068
PRIOR APPLICATION NUMBER: U.S. 60/440,757
PRIOR PELING DATE: 2003-01-14
PRIOR PELING DATE: 2003-01-14
PRIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 823
SOFTWARE: Patent In version 3.2
SEQ ID NOS: 823
SECULING DATE: 2003-05-12
SEQ ID NOS: 823
SECULING DATE: 2003-05-12
SEQ ID NOS: 823
SEQ ID NOS: 823
106 LeuProTrpValProProAspThrLysLeuSerLysLeuAspThrLeuArgLeuAlaSer 125
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Sequence 97, Application US/10247671
Publication No. US20030194721A1
GENERAL INFORMATION:
APPLICANT: Mitia, Thomas
APPLICANT: Shiffman, Dov
APPLICANT: Shiffman, Dov
PORTER: Matthew R.
TITLE OF INVENTION: GENES EXPRESED IN TREATED FOAM CELLS
FILE PEFRENCE: PA-0050 US
CURRENT APPLICATION NUMBER: US/10/247,671
FRICH RAPLICATION NUMBER: 60/323,784
PRIOR PRILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 186
SOUTWARE: PERL PROGRAM
SEQ ID NO 97
LENGTH: 2177
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; OTHER INFORMATION: Incyte ID No. US20030194721A1 3282941CB1
US-10-247-671-97
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Matches:
Conservative:
Mismatches:
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                                          126 SerTyrileAlaHisLeuArgGln 133
                                                                                     446 AGTTACATCGCTCACCTGCGGCAG 469
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Best Local Similarity:
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US-10-247-671-97
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Publication No. US20040175743A1
| Publication No. US20040175743A1
| APPLICANT: Wyeth
| APPLICANT: Burczynski, Michael
| APPLICANT: Twine, Natale
| APPLICANT: Trepication, Millie
| TILE REFERENCE: AM101080 (031896-013000)
| CURRENT FILING DATE: 2004-02-11
| NUMBER OF SEQ ID NOS: 5278
| SOFTWARE: Patentin version 3.2
| SEQ ID NO 201
| LENGTH: 1716
       APPLICANT: Hyseq. Inc.
ITILE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
ITILE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REPERENCE: 20411-756
CURRENT APPLICATION.NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
FRIOR APPLICATION NUMBER: US/09/235,076
FRIOR APPLICATION NUMBER: US/09/235,076
FRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 11181
LENGTH: 493
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Matches:
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) OTHER INFORMATION: n = A,T,C or G

US-09-918-995-11181
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US-10-775-169-201
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Best Local Similarity:
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Pred. No.:
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US-09-701-674A-23 (1-179) x US-09-908-975-134 (1-65)
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Query Match:
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; OTHER INFORMATION: Incyte ID No. US20030119009A1 3282941CB1
US-10-084-817-120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-084-817-120
| Sequence 120, Application US/10084817
| Publication No. US20030119009A1
| GENERAL INFORMATION:
| APPLICANT: Susan Stuart | APPLICANT: Jed G. Wichtern | APPLICANT: Sharon E. Plon | APPLICANT: Sharon Shohet | TITLE OF INVENTION: GENER REGULATED BY MYCN ACTIVATION | TITLE OF INVENTION UNBER: US/10/084,817 | CURRENT APPLICATION NUMBER: US/10/084,817 | CURRENT APPLICATION NUMBER: 60/270,784 | PRIOR APPLICATION NUMBER: 60/270,784 | PRIOR PELING DATE: 2001-02-23 | NUMBER OF SEQ ID NOS: 365 | SOFTWARE: PER PROGRAM | SEQ ID NOS: 365 | SEQ ID NO 120 | LENGTH: 2196 | LENGTH: 2196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: SHIFFMAN, DOV
APPLICANT: SOMGATI, Roland
APPLICANT: LAWN, Richard M.
APPLICANT: BELLHAMER, Jeffrey J.
APPLICANT: PORTER, Gordon J.
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US-10-240-965-83
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US-998-975-134

US-908-975-134

US-908-975-134

Dublication No. US20030165843A1

GENERAL INFORMATION:

APPLICANT: WASSERMAN, Alon

APPLICANT: WASSERMAN, Alon

APPLICANT: MINIZ, Eli

APPLICANT: MINIZ, Liat

APPLICANT: MINIZ, Eli

APPLICANT: MINIZ, Eli

APPLICANT: MINIZ, Eli

APPLICANTON: COLGONICLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE

CURRENT FILING DATE: 2001-07-20

CURRENT FILING DATE: 2001-07-20

PRIOR FILING DATE: 2001-05-02

PRIOR FILING DATE: 2000-07-28

PRIOR FILING DATE: 2000-07-28

NUMBER OF SEQ ID NOS: 32337

SOUTHARE PATENTING DATE: PATENTING DATE: DATE CONTO. 2000-07-28

SEQ ID NO 134

LENGTH: 65
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APPLICANT: MIKITA, Thomas
APPLICANT: TAI, Julie
TITLE OF INVENTION: GENES EXPRESSED IN FOAM CELL DIFFERENTIATION
TITLE OF INVENTION: GENES
FILE REPERENCE: PA-0025 PCT
CURRENT APPLICATION NUMBER: US/10/240,965
CURRENT PAPLICATION NUMBER: 60/195,106
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 276
SOFTWARE: PERL PROGRAM
SOFTWARE: PERL PROGRAM
TYPE: DNA
TYPE: DNA
OGGANISW: HOMO Gapiens
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; OTHER INFORMATION: Incyte ID No. US20030165924A1 977552.1
US-10-240-965-83
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ORGANISM: Rattus norvegicus
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Search completed: December 17, 2004, 04:20:36 Job time : 549 secs

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782 bp mRNA linear EST 05-AUG-2003
UI-HF-ETO-awj-c-15-0-UI.rl NIH_MGC_214 Homo sapiens cDNA clone
IMAGE:30557534 5', mRNA sequence.
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UI-HF-ETO
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Contact: Soares, MB
Cordinated Laboracory for Computational Genomics
Coordinated Laboracory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 315 8250
Fax: 319 315 8265
Email: bento-soares@uiowa.edu
Tissue Procurement: Mary Hendrix
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Distribution: Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/humanfil.html
The following repetitive elements were found in this CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo. 1 (Dases 1 to 712)
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Normalization and subtraction: two approaches to facilitate
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1 MSTGSLSDVBDLQEVEMLEC......PESDLKEVVTASRLCGTTAS 179
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            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
                                                                nucleic search, using frame_plus_p2n model
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Matches:
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EST 06-FEB-2003

linear

796 bp

BX107489

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E 1 (Gases 1 to 796)

Radelof, U., Schneider, D. and Korn, B.

Radelof, U., Schneider, D. and Korn, B.

Human UnigeneSet - RZPD3

Contact: Ina Rolfs

Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany

RZPD; INAGD998N24234.

RZPD; INAGD998N24234.

RZPD; INAGD998N24234.

RZPD; INAGD98N24234.

RZPD; INAGD8N24234.

RZPD; INAGD8N2424.

RZPD; INAGD8N24.

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RZPD; INA
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Mammalia; Eutheria; Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 796)
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BX107489 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGP998N24234 ; IMAGE:151511, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .796
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/mol_type="mRNA"
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/sex="Female"
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Best Local Similarity:
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Homo sapiens
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100

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337

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457

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Submitted (20-701-2004) Genoscope - Centre National de Sequencage : BP 191 91006 BYRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr) a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pcMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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1 (bases 1 to 1221)
11, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            161 GluSerAspLeuLysGluValValThrAlaSerArgLeuCysGlyThrThrAlaSer 179
                                                                                                                                                                                           CGCAACGCCGCCAACGCGCGCAAGAGCGGGCCCGCATGCGAGGTGCTGAGCAAGGCCTTCTCCC
                                                                              1 MetSerThrGlySerLeuSerAspValGluAspLeuGlnGluValGluMetLeuGluCys
                                                                                                           21 AspGlyLeuLysMetAspSerAsnLysGluPheValThrSerAsnGluSerThrGluGlu
                                                                                                                                                                                                                                                   SerSerAsnCysGluAsnGlySerProGlnLysGlyArgGlyGlyLeuGlyLysArgArg
                                                                                                                                                                                                                                                                                                                                   LysAlaProThrLysLysSerProLeuSerGlyValSerGlnGluGlyLysGlnValGln
                                                                                                                                                                                                                                                                                                                                                                           458 AAGGCGCCCACCAAGAAGAGCCCCCTGAGCGGGGGTCAGCCAGGAGGGGAAGCAGGTCCAG
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http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
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CR594669 1 GI:50475476
HTC; CNSLT CDNA.
HOMC saplens (human)
Homc saplens
                                          US-09-701-674A-23 (1-179) x AL550251
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E. (Data to Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization

D. Pull-length cDNA libraries and normalization

D. Prob 15, 2001 this sequence version replaced gi:31272068.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr. Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was disested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT c vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALS50251 1044 bp mRNA linear EST 25-MAR-2004
ALS50251 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
Clone (SODI039YJ05 5-PRIME, mRNA sequence.
ALS50251
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80
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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized.
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                                                                                                                                                                                           AGACTCAAGACCACCCTGCCTGGGTGCCCCCGGACACCAAGCTCTCCAAGCTGGACACG
LysAlaProThrLysLysSerProLeuSerGlyValSerGlnGluGlyLysGlnValGln
                                          AAGGCGCCCCACCAAGAAGAGCCCCCTGAGCGGGGTCAGCCAGGAGGGGAAGCAGGTCCAG
                                                                                  ArgAsnAlaAlaAsnAlaArgGluArgAlaArgMetArgValLeuSerLysAlaPheSer
                                                                                                                        ArgleulysThrTeuProTrpValProProAspThrLysLeuSerLysLeuAspThr
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/organism="Homo sapiens"

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Direct Submission
Submitted (20-JUM-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
184 b: www.genoscope.cns.fr)
184 strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitogen.
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1 (bases 1 to 1250)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGTCCACCGGCTCCCTCAGCGATGTGGAGGACCTTCAAGAGGTGGAGATGTTGGAATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                         ArgAsnAlaAlaAsnAlaArgGluArgAlaArgMetArgValLeuSerLysAlaPheSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        560 AGACTCAAGACCACCTGCCCTGGCCCCCCGACACCAAGCTCTCCAAGCTGGACACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTCAGGCTGGCTCCAGCTACATCGCCCACTTGAGGCAGATCCTGGCTAACGACAAATAC
                                                                                                                                                                                                                                                                                                                                   320 GACGGGTTGAAATGGATTCGAACAAGGAATTTGTGACTTCCAACGAGGAGCACCGAGGAG
                                                                                                                                                                                                                                                                                                                                                        41 SerSerAsnCysGluAsnGlySerProGlnLysGlyArgGlyGlyLeuGlyLysArgArg
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                                                                                                                                                                                                                                                                                                         AspGlyLeuLysMetAspSerAsnLysGluPheValThrSerAsnGluSerThrGluGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact : Feng Liang Bmail : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
/mol_type="mRNA"
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                                                                                                                1221
179
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Mismatches:
Indels:
                                                                                                                  Length:
Matches:
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HTC; CNSLT CDNA.
Homo sapiens (human)
Homo sapiens
                                                                                                                  4.54e-169
179.00
100.00%
100.00%
100.00%
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Best Local Similarity:
Query Match:
DB:
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DEFINITION
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CR606057
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CR616308 1252 bp. mRNA linear HTC 21-JUL-2004 full-length cDNA clone CS0DI070YK16 of Placenta Cot 25-normalized of Homo sapiens (human).
CR616308 CR616308.1 GI:50497115
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                                                                                                                                                                                                                                                                                                                                                                                                             21 AspGlyLeuLysMetAspSerAsnLysGluPheValThrSerAsnGluSerThrGluGlu
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1. 1250

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                                                                                                                                                                                                   1250
179
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Matches:
Conservative:
Mismatches:
Indels:
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/clone|lb="mNH MGC|l25"
/note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;
/note="Organ: ovaries; from females ranging in age from 38 to of threaty is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 036."
                                                                                                                                                                                            BM544256 1038 bp mRNA linear EST 20-FEB-2002
AGENCOURT 6490671 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5587760
5', mRNA sequence.
BM544256
         692 GAGAACGGGTACATTCACCCGGTCAACCTGACGTGGCCCTTTATGGTGGCCGGGAAACCC 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82 TCCACCGGCTCCCTCAGCGATGTGGAGGACCTTCAAGAGGTGAGATGTTGGAATGTGAC 141
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1038)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Enail: cgapbs-remail.nih.gov
Tissue Procurement: Invitrogen
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llh.gov
Plate: LLAM12357 row: m column: 09
High quality sequence stop: 774.
                                                    161 GluSerAspLeuLysGluValValThrAlaSerArgLeuCysGlyThrThrAlaSer 179
                                                                                 SerAsnCysGluAsnGlySerProGlnLysGlyArgGlyGlyLeuGlyLysArgArgLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                  Genoscope.

Direct Submission

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a Not1-oligo(dT) primer. Five prime den cirched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMV8PORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  272 ATGICCACCGGCTCCCTCAGCGAIGTGGAGGACCTTCAAGAGGTGGAGATGTTGGAATGT 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    332 GACGGGTTGAAAATGGATTCGAACAAGAATTTGTGACTTCCAACGAGGGGG 391
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                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1. (bases 1 to 1252) 1. (bases 1 to 1252) 1. (Br. Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81 ArgasnalaasnalaargGluargalaargMetargValLeuSerLysAlaPheSer
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                                                                                                                                                                                                             Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="Heaxon:9606"
/clone="CSODIO70YK16"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"
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179
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HTC; CNSLT_cDNA.
Homo sapiens (human)
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pel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is GATAAGGCCA. Tissue was provided by Mary Hendrix."
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AL552119 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA AL552119 Homo sapiens CDNA AL552119 GINS9VH17 5-PRIME, mRNA sequence.

AL552119
AL552119.3 GI:45856508
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Li W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Ombublished (2001)
On Feb 15, 2001 this sequence version replaced gi:31273935.
Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        678 dagaacegeracarrcacceegrcaaccreacereececcrrrareereececesaaacce
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Contect: Soares, MB
Contect: Soares, MB
Content de Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 9265
Fax: 319 335 9265
Fax: 319 335 9265
Fax: 319 335 9265
Email: bento-soares@uiowa.edu
Tissue Procurement: Mary Hendrix
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
CLONE Distribution Distribution information can be found at
http://genome.uiowa.edu/distribution/humanfl.html
The following repetitive elements were found in this cDNA
sequence: 172-253, >(GA)n#Simple_repeat (matched compliment)
Seq prime: pXx-5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGC_214 Homo sapiens cDNA clone
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30554533"
/tissue_type="Chondrosarcoma Lung Metastasis cell lines"
/tissue_type="Chondrosarcoma Lung Metastasis cell lines"
/lab_host="DH10B (TI phage resistant)"
/clone_lib="NH1 MGC 214"
/note="Organ: Lung, Vector: pYX-Asc, Site 1: EcoR I;
Site 2: Not 1, The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarcse
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1 (bases 1 to 800)
Bonaldo, M. F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                AsnGlyTyrIleHisProValAsnLeuThrTrpProPheMetValAlaGlyLysProGlu
                                                                                                                  82 AsnAlaAsnAlaArgGluArgAlaArgMetArgValLeuSerLysAlaPheSerArg
                                                                                                                                         LeuLysThrThrLeuProTrpValProProAspThrLysLeuSerLysLeuAspThrLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                  502 AACGGGTACATTCACCCGGTCAACCTGACGTGGCCCTTTATGGTGGCCGGGAAACCCGAG
                               AlaProThrLysLysSerProLeuSerGlyValSerGlnGluGlyLysGlnValGlnArg
                                                                       262 gegeceaecaagaagageceeergagegggeggreageeagggggagggaggaggreagee
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UI-HF-ETO-awh-f-14-0-UI.rl NIH_MGC
IMAGE:30554533 5', mRNA sequence.
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EST 30-MAR-2004

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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a Not1-oligo(dT) Frimer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pcMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
3812.f
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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     320 GACGGGTTGAAAATGGATTCGAACAAGGAATTTGTGACTTCCAACGAGGCACCGAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 AspGlyLeuLysMetAspSerAsnLysGluPheValThrSerAsnGluSerThrGluGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SerSerAsnCysGluAsnGlySerProGlnLysGlyArgGlyGlyLeuGlyLysArgArg
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Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity:
Query Match:
DB:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 965)

1 (bases 2 to 965)

1 (bases 2 to 965)

1 (bases 3 to 965)

1 (bases 2 to 965)

1 (bases 2 to 965)

1 (bases 2 to 965)

1 (bases 3 to 966)

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         MENA linear EST 30-MAR-200 COT 25-NORMALIZED Homo sapiens CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         forgatism="Homo sapiens"
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primer. Five prime and enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and BCOR V
sites of the pCMVSPORT 6 vector. Library was normalized.
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175
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AL552380 mRNA 5455 bp mRNA 5455280 HOMO Sapiens PLACENTA COT 25-NORM Clone CSODI070YK16 5-PRIME, MRNA Sequence AL552380
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MGC_214 Homo sapiens cDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 757)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                               268 ATGTCCACCGGCTCCCTCAGCGATGTGGAGGACCTTCAAGAGGTGGAGATGTGTAATGTTGGAATGT
                                                                                                                                                              41 SerSerAsnCysGluAsnGlySerProGlnLysGlyArgGlyGlyLeuGlyLysArgArg
                                                                                                                                                                                           448 AAGGCGCCCACCAAGAAGAGCCCCCTGAGCGGGGTCAGCCAGGAGGGGGAAGCAGGTCCAG
                                                                                                                                                                                                                                                                                                                                             ArgAsnAlaAlaAsnAlaArgGluArgAlaArgMetArgValLeuSerLysAlaPheSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AspGlyLeuLysMetAspSerAsnLysGluPheValThrSerAsnGluSerThrGluGlu
                                                                                                                                                                                                                                                    61 LysAlaProThrLysLysSerProLeuSerGlyValSerGlnGluGlyLysGlnValGln
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The following repetitive elements were found in this cDNA Sequence: 1977-258, (GA)n#Simple_repeat (matched compliment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEBRF, Iowa City, IA 52242,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     141 GluAsnGlyTyrIleHisProValAsnLeuThrTrpPro 153
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UI-HP-ETD-avx-k-09-0-UI.rl NIH MG
IMAGE:30563480 5', mRNA sequence.
CF126927 GF:33204654
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97044477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             location/Qualifiers
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AUTHORS
TITLE
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PUBMED
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="intaxon:9606"
/clone="intaxon:9606"
/lone="intaxon:9606"
/lone="intaxon:pooled colon, kidney, stomach, Vector:
/note="Organ: pooled colon, kidney, stomach, Vector:
pcMv-SpoRT6; Site=1: Not1; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1.3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."
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Bukaryota; Ito 1098)

Bu (bases Ito 1098)

NH-MGC http://mgc.nci.nih.gov/.

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llh.gov

High quality sequence stop: 693.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                  AGENCOURT 6626079 NIH_MGC_116 Homo sapiens CDNA clone IMAGE:5758942
                                                                                                                                           141 GludanGlyTyrIleHisProValAsnLeuThrTrpProPheMetValAlaGlyLysPro 160
                                                                                                                                                                                        692 GAGAACGGGTACATTCACCCGGTCAACCTGACGTGGCCCTTTATGGTGGCCGGGAAACC- 750
                                                                                               691
       572 AGACTCAAGACCACCCTGCCCTGGGTGCCCCCGACACCCAAGCTCTCCAAGCTGGACACG
                                                  121 LeuargLeualaSerSerTyrIlealaHisLeuargGlnIleLeualaAspLysTyr
                                                                                             632 CICAGGCIGGCGICCAGCIACAICGCCCACIIGAGGCAGAICCIGGCIAACGACAAIAC
                                                                                                                                                                                                                                   161 GluSerAspLeuLysGluValValThrAlaSerArgLeuCysGlyThr 176
                                                                                                                                                                                                                                                              751 GAGAGTGACCTGAAAGAAGTGGTGACCGCGAGCCGCTTATGTGGAACA 798
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Mismatches:
Indels:
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Query Match:
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BM923344
LOCUS
DEFINITION
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TITLE
JOURNAL
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REFERENCE

FEATURES

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1 MetSerThrGlySerLeuSerAspValGluAspLeuGlnGluValGluMetLeuGluCys 20

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                           Email: cgapbs-remail.mih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI1513 row
High quality sequence stop: 744.
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Matches:
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        Contact: Robert Strausberg, Ph.D.
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/lab_host="DH10B (TI phage resistant)"
/clone lib="MIH MGC 214"
/noce="Organ: Lung; Vector: pXx.Asc; Site 1: EcoR I;
Site 2: Nct I; The library was constructed according
Site 2: Nct I; The library was constructed according
BonalGo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarcs
gel. First strand CDNA synthesis was primed with oligo-dr
primer containing a Not I site. Double strand CDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with Not I and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is GATAAGGCCA. Tissue was provided by Mary Hendrix."
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1 (bases 1 to 746)
NHI-MGC http://mgc.nci.nih.gov/.
NAIL-OTA Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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BI770998
BI770998.1 GI:15762576
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Homo sapiens
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Rest Local Similarity:
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DEFINITION

ACCESSION

RESULT 14 CF128246

AUTHORS TITLE

REFERENCE

MEDLINE PUBMED

COMMENT

JOURNAL

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Coordinated Laboratory for Computational Genomics
Coordinated Laboratory for Computational Genomics
University of Iowa
77 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
78 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
79 135 9856
Fax: 319 335 9856
Fax: 319 335 9856
Fax: 319 335 9856
Fax: 419 335 9856
Fax: 419 185 9856
Fax: 419 135 9856
Fax: 419 135 9856
Fax: 419 135 9856
Fax: 419 185 9856
Fax: 41
125 ATGTCCACCGGCTCCCTCAGCGATGTGGAGCACCTTCAAGAGGTGGAGATGTTGGAATGT 184
                                                                                 1. 744

Organism="Homo sapiens"

(mol_type="mRMA" |

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/tissue_type="Chondrosarcoma resistant" |

/clone_lib="NIH_MGC_214"

/note="Crgan: Lung; Vector: pYX-Asc; Site_1: EcoR I;

/note="Crgan: Lung; Vector: pYX-Asc; Site_1: EcoR I;

Site_2: Not I; The library was constructed according

Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukarrota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Primates; Catarrhini, Hominidae; Homo. I (Bases I to 74. Enno. Bonaldo, M.F., Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                               245 Agerceaacreceaeaaregercreeceaaagegeceeceeceeceaeaea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CF128914 The TOP-09-0-UI.rl NIH MGC_214 Homo sapiens CDNA clone IMAGE:30563216 5', mRNA sequence.
                                                     21 AspGlyLeuLysMetAspSerAsnLysGluPheValThrSerAsnGluSerThrGluGlu
                                                                                                                                                                          SerSerAsnCysGluAsnGlySerProGlnLysGlyArgGlyGlyLeuGlyLysArgArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 LeuargLeualaSerSerTyrIlealaHisLeuargGlnIleLeualaAsnAsp 138
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The following repetitive elements were found in this cDNA
sequence: 191-272, > (GA) n#Simple_repeat (matched compliment)
Seq primer: pXx-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTCAGGCTGGCGTCCAGCTACATCGCCCACTTGAGGCAGATCCTGGCTAACGAC
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CF128914.1 GI:33208641
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Homo sapiens
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Fax: 319 318 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Mary Hendrix
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/humanfl.html
The following repetitive elements were found in this CDNA sequence: 39-120, > (GA)n#Simple_repeat (matched compliment)
                                                                                                                                                    CF128246

HOT-HF-ETO-awf-c-24-0-UI.r1 NIH_MGC_214 Homo sapiens cDNA clone IMAGE:30555623 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 645)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Coordinated Laboratory for Computational Genomics
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30555623"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome Res. 6 (9), 791-806 (1996)
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Location/Qualifiers
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CF128246.1 GI:33207297
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      oGluSer 162
                                                           738 CGAGAGT 744
                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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FEATURES

MetSerThrGlySerLeuSerAspValGluAspLeuGlnGluValGluMetLeuGluCys 20

Pred. No.:

Best Local

EST 05-AUG-2003

484

120

100

424

364

80

304

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1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I and then cloned directionally into pXX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is GATAAGGCCA. Tissue was provided by Mary Hendrix."
```

ORIGIN

4.65e-128 Length: 744 138.00 Matches: 138 100.00\$ Conservative: 0 100.00\$ Mismatches: 0 77.09\$ Indels: 0 6	9) x CF128914 (1-744)	31ySerLeuSerAspValGluAspLeuGluGluValGluMetLeuGluCys 20	AIGTCCACCGGCTCCCTCAGCGATGTGGAGGACCTTCAAGAGGTGGAGATGTTGGAATGT 336	AspGlyLeuLysMetAspSerAsnLysGluPheValThrSerAsnGluSerThrGluGlu 40	GACGGGTTGAAAATGGATTCGAACAAGGAATTTGTGACTTCCAACGAGAGCACCGAGGGG 396	SerSerAsnCysGluAsnGlySerProGlnLysGlyArgGlyGlyLeuGlyLysArgArg 60	AGCTCCAACTGCGAGAATGGGTCTCCCCAGAAGGCCCGCGGCGCGCGTGGGCAAGAGGAGGGGGG	ThrLysLysSerProLeuSerGlyValSerGlnGluGlyLysGlnValGln 80	AAGGCGCCCAACAAGAGAGCCCCCTGAGCGGGGTCAGCAGGGGGGAAGCAGCAGCTCCAG 516	ArgAsnAlaAlaAsnAlaArgGluArgAlaArgMetArgValLeuSerLysAlaPheSer 100 '	GCCAACGCCGCCAACGCGCGAGGGGGCCGCATGCGAGGCTGCTGAGGCAAGGCTTCTCC 576	ArgleuLysThrThrLeuProTrpValProProAspThrLysLeuSerLysLeuAspThr 120	AGACTCAAGACCACCCTGCCCTGGGTGCCCCCCGACACCAAGCTCTCCCAAGCTGGGACACG 636	LeuArgLeuAlaSerSerTyrileAlaHisLeuArgGlnileLeuAlaAsnAsp 138	COV
ity:	-23 (1-179)	MetSerThrGl	ATGTCCACC	AspGlyLeuI	GACGGGTTGA	SerSerAsnC	AGCTCCAACT	LysAlaProThrLy	AAGGCGCCCA	ArgAsnAlaA	CGCAACGCCG	Argleulysī	AGACTCAAGA	LeuArgLeuA	
	US-09-701-674A-23	H	277	21	337 (	41	397	61 ]	457	81 7	517	101	577	121	
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Search completed: December 17, 2004, 03:13:22 Job time : 2874 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Total number of hits satisfying chosen parameters:

seg length: 0 seg length: 200000000

Minimum DB Maximum DB

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

parameters:

Database

4093002 seqs, 2760418825 residues

0.5 7.0 7.0

, Xgapext , Ygapext , Fgapext , Delext

Xgapop 10.0, Ygapop 10.0, Fgapop 6.0, Delop 6.0, BLOSUM62

US-09-701-674A-23 917 1 MSTGSLSDVEDLQEVI

Title: Perfect score:

Run on:

Sequence:

Scoring table:

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Sequence 1307, App
Sequence 27, Appl
Sequence 201, Appl
Sequence 30, Appl
Sequence 365, Appl
Sequence 365, Appl
Sequence 1028, Appl
Sequence 1028, Appl
Sequence 1028, Appl
Sequence 1028, Appl
Sequence 11181, Appl
Sequence 227, Appl
Sequence 227, Appl
Sequence 251, Appl
Sequence 251, Appl
Sequence 2740, Appl
Sequence 106, Appl
Sequence 106, Appl
Sequence 106, Appl
Sequence 106, Appl
Sequence 65, Appl
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Sequence 63, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 35, Appl
Sequence 35, Appl
Sequence 194, Appl
                       Description
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Sequence 1307, Application US/10264049
Fublication No. US2004000557941
GENERAL INFORMATION:
APPLICANT: Birse et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA133P1
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: US/10/264,049
FRIOR APPLICATION NUMBER: PCT/US01/18569
PRIOR PILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: US 60/209,467
PRIOR FILING DATE: 2000-06-07
SOFTWARE PELACOTION NUMBER: US 60/209,467
PRIOR FILING DATE: 2000-06-07
SOFTWARE PELACOTION NUMBER: US 60/209,467
FRIOR FILING DATE: 2000-06-07
SOFTWARE PATENTIN VOICE: 3.1
ENGIH: 632
                                                  5 US-10-264-049-1307
5 US-10-244-671-97
5 US-10-240-965-93
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ORGANISM: Homo sapiens
FEATURE:
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No.
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1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/Per_Naw Pubs.seq:*
3: /cgn2_6/ptodata/1/pubpna/USO6_NEW Pubs.seq:*
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19: /cgn2_6/ptodata/1/pubpna/USO0P_NEW PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                         NAME/KEY: misc feature
LOCATION: (1747)...(174)
TOTHER INFORMATION: n equals a,t,g, or
FEATURE: nisc feature
LOCATION: (2317)...(231)
OTHER INFORMATION: n equals a,t,g, or
FEATURE: misc feature
LOCATION: (245)...(249)
OTHER INFORMATION: n equals a,t,g, or
OTHER INFORMATION: n equals a,t,g, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: misc feature
LOCATION: (629)
. COTHER INFORMATION: n equals a,t,g,
LOCATION: (78) .. (79)
OTHER INFORMATION: n equals a,t,g,
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: misc_feature
LOCATION: (331)..(331)
OTHER INFORMATION: n equals a,t,g,
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LOCATION: (498)
JTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: misc_feature
LOCATION: (537). (537)
OTHER INFORMATION: n equals a,t,g,
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LOCATION: (623)..(623)
OTHER INFORMATION: n equals a,t,g,
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NAME/KEY: misc_feature
LOCATION: (280)..(280)
OTHER INFORMATION: n equals a,t,g,
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NAME/KEY:
LOCATION: (552)..(552)
OTHER INFORMATION: n equals a,t,g,
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764.50
91.62%
91.06%
83.37%
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LOCATION: (265)...(265)
OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals
FEATURE:
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LOCATION: (546)...(546)
OTHER INFORMATION: n equals
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NAME/KEY: misc feature
LOCATION: (263)...(263)
OTHER INFORMATION: n equals
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LOCATION: (433)...(433)
OTHER INFORMATION: n equals
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Best Local Similarity:
Query Match:
DB:
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101 ArgieulysThrThrleuProTrpValProProAspThrLysLeuSerLysLeuAspThr 120
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                                                                                                          21 AspGlyLeuLysMetAspSerAsnLysGluPheValThrSerAsnGluSerThrGluGlu 40
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                                                                  13 ATGTCCACCACTCCCTCAGCGATGTGGAGGACCTTCAAGAGGTGGAGATGTTGGAATGT
                                                                                                                                            73 GACGGINTGAAATGGATTCGAACAAGGAATTTGTGACTTCCAACGAGGAGCGACGAGGAG
                                                                                                                                                                                      41 SerSerAsnCysGluAsnGlySerProGlnLysGlyArgGlyGlyLeuGlyLysArgArg
                                                                                                                                                                                                                    61 LysAlaProThrLysLysSerProLeuSerGlyValSerGlnGluGlyLysGlnValGln
                                                                                                                                                                                                                                                                                                                                          81 ArgAsnAlaAsnAlaArgGluArgAlaArgMetArgValLeuSerLysAlaPheSer
                                                                                                                                                                                                                                                                                                                                                                                                                                            313 AGACTCAAGACCACCCTGNCCTGGCTGCCCCCGACACCACACTCTCCAAGCTGGACACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141 GluAsnGlyTyrileHisProValAsnLeuThrTrpProPheMetValAlaGlyLysPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  433 NAGAACGGCTACATTA--CCCGGGCAACTGACGTGGNCCTTTATGGTGGC-GGGAAACCC
                                      1 MetSerThrGlySerLeuSerAspValGluAspLeuGlnGluValGluMetLeuGluCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          161 GluSerAspleuLysGluValVal-ThrAlaSerArgLeuCysGlyThrThrAla 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              490 GAGAGTGANCTGAAGAAGTGGTTGACCGCGAGCCGGTTATGTGGAANCACCGCG 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 97, Application US/10247671

Sequence 97, Application US/10247671

Publication No. US20030194721A1

GENERAL INFORMATION:
APPLICANT: Mixita, Thomas
APPLICANT: Mixita, Thomas
APPLICANT: FASSET, MARCHEW R.
TITLE REPERENCE: PA-0050 US
CURRENT APPLICATION NUMBER: US/10/247,671

CURRENT APPLICATION NUMBER: US/10/247,671

CURRENT APPLICATION NUMBER: 60/323,784

PRIOR APPLICATION NUMBER: 60/323,784

PRIOR FILING DATE: 2001-09-19

NUMBER OF EXQ ID NOS: 186

SOFTWARE: PERL PROGram

SEQ ID NO 97

LENGTH: 2177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE: ..... - FEATURE: NAME/KEY: misc_feature ; OTHER INFORMATION: Incyte ID No. US20030194721A1 3282941CB1 US-10-247-671-97
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Matches:
Conservative:
Mismatches:
Indels:
US-09-701-674A-23 (1-179) x US-10-264-049-1307 (1-632)
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514.00
63.21%
53.30%
56.05%
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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US-10-247-671-97
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Score: 514.00 Matches: 113 Percent Similarity: 63.21\$ Conservative: 21 Best Local Similarity: 53.30\$ Mismatches: 38 Query Match: 56.05\$ Indels: 40 DB: 640	US-09-701-674A-23 (1-179) x US-10-084-817-120 (1-2196)	Oy 1 MetSerThrGlySerLeuSerAspValGluAspLeuGlnGluValGluMetLeuGluCys 20	Qy 21 AspGlyLeuLys	Qy 26 AspSerAsnLysGluPheValThrSerAsnGluSerThrGluGlu	SerSerAbnCygCluAsnGlySer         :::         :::   AGCGCTGCGCTCTGGGCACGCACGCGGAAGGCTGCAAGAGGAAGGGG	49 ProGlnLysGlyArgGlyGlyLysArgArgArgLysAlaProThrLysLysSer 6	68ProLeuSerGlyValSerGlnGluGlyLysGlnValGlnArgAsnAlaAsnAla 86	Qy 87 ArgGluArgAlaArgWetArgValLeuSerLysAlaPheSerArgLeuLysThrThrLeu 106	Oy 107 ProTrpValProProAspThrLysLeuSerLysLeuAspThrLeuArgLeuAlaSerSer 126	Oy 127 TyrilealahiseLeuArgGlnileLeuAlaAsnAspLysTyrGluAsnGlyTyrileHis 146	Qy 147 ProvalAsnLeuThrTrpProPheMetValAlaGlyLysProGluSerAspLeuLysGlu 166	Oy 167 ValValThrAlaSerArgLeuCysGlyThrThrAla 178	RESULT 4 US-10-240-965-83 ; Sequence 83, Application US/10240865	; Publication No. US20030165924A1 ; GENERAL INFORMATION: ; APPLICANT: INCYTE GENOMICS, INC.	; APPLICANT: SHIFFMAN, Dov ; APPLICANT: SOMOGYI, Roland ; APPLICANT: LAWN, Richard M.	; APPLICANT: SELHAMER, Jeffrey J. ; APPLICANT: PORTER, Gordon J. ; APPLICANT: MITTA, Thomas ; APPLICANT: MITTA, Thomas	; TITLE OF INVENTED SERVICES EXPRESSED IN FOAM CELL DIFFERENTIATION : FILE REFERENCE: PA-0025 PCT	CURRENT APPLICATION NUMBER: US/10/240,965 ; CURRENT FILING DATE: 2002-10-04 ; PRLOR APPLICATION NUMBER: 60/195,106 ; DELOR PILING DATE: 2000-04-06	; NUMBER OF SEQ ID NOS: 276 ; SOFTWARE: PERL Program
1 MetSerThrGlySerLeuSerAspValGluAspLeuGlnGluValGluMetLeuGluCys 2	Qy 21 AspolyLeuLys	26 AspSerAsnLysGluPheValThrSerAsnGluSerThrGluGlu	DB SeU GAGCGCAGCTACGCCTCGCCCAGIGACAACICGTCGGCAGAGGAGGACGCCCGAGGGC 519 QY 41	### ### ##############################	68ProLeuserGlyValSerGlnGluGlyLyGlnValGlnArgAsnAlaAsnAla 86	87 ArgGluArgAlaArgMetArgValLeuSerLysAlaPheSerArgLeuLysThrThrLeu 10	Oy 107 ProTrpValProProAspThrLysLeuSerLysLeuAspThrLeuArgLeuAlaSerSer 126	Oy 127 TyrilealamisheuargginileheualaashaspiysTyrgluasnglyTyrilehis 146	147 ProValAsnLeuThrTrpProPheMetValAlaGlyLysProGluSerAspLeuLysGlu 16	167 ValValThrAlaSerArgLeuCysGlyThrThrAla 178  167 ValValThrAlaSerArgLeuCysGlyThrThrAla 178  1040 GTTTCGCAGCGAACAGACTAGGAACCAGCAGGAACAGAACCAACGAACAGAACAGAACAGAACAGAACAGAACAGAACAGAACAGAACAGAACAAGAAAAAA	SULT 3	; Sequence 120, Application US/1008481/ ; Publication No. US20030119009A1 ; GENERAL INFORMATION: ; APPLICANT: Susan Stuart	; APPLICANT: Jed G. Nuchtern ; APPLICANT: Sharon E. Plon ; APPLICANT: Jason M. Shohet ; TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION	FILE REFERENCE: PA-0046 US CURRENT APPLICATION NUMBER CURRENT FILING DATE: 2002	; PRIOR APPLICATION NUMBER: 60/270,784 ; PRIOR FILING DATE: 2001-02-23 ; NUMBER OF SEQ ID NOS: 365	; SOFTWARE: PERL Program ; SEQ ID NO 120 ; LENGTH: 2196 ; TAPE. DATA		S-1	Alignment Scores: Pred. No.: 3.34e-54 Length: 2196

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TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           503 CGGGGGTCCAGCGGGAGTACCCGGCTCCAAGAGGCCGCCCTCCGCGGGGTA 562
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40 GluSerSerAsnCysGluAsnGlySerProGlnLysGlyArgGly-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 AspSerAsnLysGluPheValThrSerAsnGluSerThrGlu-----
                                       TYPE: DNA
OGGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20030165924A1 977552.1
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           161 ATGTCCACGGGCTCGGTGAGTGATCCGGAGGAG-
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Sequence 201, Application US/10775169
Sequence 201, No. US20040175743A1
SENERAL INFORMATION:
HAPLICANT: Wyeth
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Twine, Natalie
Dorner, Andrew
Trepicchio, William
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507.00
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Best Local Similarity:
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SEQ ID NO 83
LENGTH: 2382
                                                                                                                                               ; OTHER INFORM
US-10-240-965-83
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DB:
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110 AGTGACAACTCGTCGGCAGAGGAGGAGGACCCCGACGGCGAGGAGGGGCTGCGCTTGTG 169
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TITLE OF INVENTION: Method for Monitoring Drug Activities In 'PILE REFERENCE: AM10.1080 (03.1896-013.000)
CURRENT APPLICATION NUMBER: US/10/775,169
CURRENT FILING DATE: 2004-02-11
NUMBER OF SEQ ID NOS: 5278
SOFTWARR: ParentIn version 3.2
SOFTWARR: ParentIn version 3.2
LENGTH: 1716
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APPLICANT ALTONION Janice K.; Seilhamer, Jeffrey J.
TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expressio FILE PETERENCE: PA-0002-1 CON
CURRENT APPLICATION NUMBER: US/10/305,720
CURRENT PILING DATE: 2002-11-26
PRIOR FILING DATE: 1998-01-30
NUMBER OF SEQ ID NOS: 1490
SOFTWARE: PERL PROGRAM
SEQ ID NO 1208
LENGTH: 240
                                                                                                                                                                                                                                                                                                                                                                                                                                       107 ProTrpValProProAspThrLysLeuSerLysLeuAspThrLeuArgLeuAlaSerSer 126
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                                                                                                                                                                                                                                                                                                                                                                   ArgGluArgAlaArgMetArgValleuSerLysAlaPheSerArgLeuLysThrLeu 106
                                                                                         255 CGGGGGCTGCAGCGGGGAGTACCCGGTCCCCGCCTCCAAGAGGCCGCCCCTCCGCGGGGGTA 314
                                                                                                                                                                        315 GAGCGCAGCTACGCCTCGCCCAGTGACÁÁCTCGTCGGCAGÁGGÁGGAGGACCCCGACGGC 374
                                                                                                                                                                                                                                                                                                     ----ATGGAGCTT 254
1 MetSerThrGlySerLeuSerAspValGluAspLeuGluGluValGluMetLeuGluCys 20
                                                                                                                                                                                                                                      375 GAGGAGGAGCGCTGCGCTCTGGGCACAGCCGGGGGGGGGAAGGCTGCAAGAGGAAGCGG
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                                                                                                                                                                                                         ----SerSerAsnCysGluAsnGlySer
                                                                                                                                                                                                                                                                                                                                               68 --- ProLeuSerGlyValSerGlnGluGlyLysGlnValGlnArgAsnAlaAsnAla
                                                                                                                                   26 AspSerAsnLysGluPheValThrSerAsnGluSerThrGluGlu----
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OTHER INFORMATION: Incyte ID No. US20040010136A1 954226
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                    213 ATGTCCACGGGCTCGGTGAGTGATCCGGAGGAG---
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Sequence 1028, Application US/10305720
Publication No. US20040010136A1
GENERAL INFORMATION:
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| LOCATION: (1) ... (240)
| OTHER INFORMATION: a, t,
US-10-305-720-1028
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Pred. No.:
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TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-kB
TITLE OF INVENTION: PATHWAY
FILE OF INVENTION: PATHWAY
CURRENT APPLICATION NUMBER: US/10/755,889
CURRENT PILICAD ADAI: 2004-01-13
PRIOR APPLICATION NUMBER: U.S. 60/440,068
PRIOR PILICATION NUMBER: U.S. 60/469,757
PRIOR APPLICATION NUMBER: U.S. 60/469,757
PRIOR APPLICATION NUMBER: U.S. 60/469,757
NUMBER OF SEQ ID NOS: 823
SOFTWARE: Patent In version 3.2
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Publication No. US20040171823A1
GENERAL INFORMATION:
                j LENGTH: 482

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc_feature

COCATION: (1)...(482)

COPHER INFORMATION: n = A,T,C or G
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Best Local Similarity:
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US-10-755-889-365
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LENGTH: 1939
   SEQ ID NO 9069
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RESULT 108-09-594-456-1245

NESCULT 0. U820020115057A1

GENERAL INFORMATION:

APPLICATION:

APPLICATION:

APPLICATION WIDERS for Identifying Anti-Cancer Therapeutic Agents Using Cancer TILE REPERENCE: 69290-76

CURRENT APPLICATION WHERE: US/09/954,456

CURRENT FILING DATE: 2001-09-18

PRIOR APPLICATION WHERE: US/60/33,617

PRIOR APPLICATION WHERE: US/60/33,637

PRIOR APPLICATION WHERE: US/60/33,432

PRIOR APPLICATION WHERE: US/60/235,134

PRIOR FILING DATE: 2000-09-26

PRIOR APPLICATION WHERE: US/60/235,134

PRIOR APPLICATION WHERE: US/60/235,637

PRIOR APPLICATION WHERE: US/60/235,637

PRIOR APPLICATION WHERE: US/60/235,637

PRIOR PILING DATE: 2000-09-26

PRIOR PILING DATE: 2000-09-27

PRIOR PILING DATE
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                               US-09-701-674A-23 (1-179) x US-09-954-456-829 (1-697)
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; OTHER INFORMATION: n=a,t,g or
US-09-954-456-1245
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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APPLICANT: Voung paul

ITILE OF INVENTION: Sets

TITLE OF INVENTION: Sets

FILE REFREENCE: 66220-76

CURRENT FILING DATE: 2001-09-18

FRIOR PILING DATE: 2000-09-26

FRIOR APPLICATION NUMBER: US/60/234,923

FRIOR PILING DATE: 2000-09-26

FRIOR PILING DATE: 2000-09-26

FRIOR APPLICATION NUMBER: US/60/235,134

FRIOR FILING DATE: 2000-09-25

FRIOR PILING DATE: 2000-09-25

FRIOR APPLICATION NUMBER: US/60/235,637

FRIOR FILING DATE: 2000-09-26

FRIOR PILING DATE: 2000-09-26

FRIOR FILING DATE: 2000-09-27

FRIOR FILING DATE: 2000-09-27
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; Patent No. US20020115057A1
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OTHER INFORMATION: n=a,t,g or
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ORGANISM: Homo sapiens
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Best Local Similarity:
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US-09-954-456-829
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APPLICANT: Munger, William E.
APPLICANT: Wateri, Prakash
APPLICANT: Wateri, Prakash
APPLICANT: Getzenberg, Robert H.
APPLICANT: Waga, Iwao
APPLICANT: Yamanoro, Jun
AITLE OF INVENTION: Hyperplasia Using Gene Expression Profiles
FILE REPERBRENCE: 4921-5029-US
CURRENT APPLICATION NUMBER: US/09/873,319A
CURRENT FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 755
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 679
LENGTH: 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             159 LysProGluSerAspLeuLysGluValValThrAlaSerArgLeuCysGlyThrThrAla 178
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Sequence 11141, Application US/09918995

Publication No. US20030073623A1

GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES

TITLE OF INVENTION: NOWBER: US/09/918,995

CURRENT FILITG DATE: 2001-07-30

PRIOR APPLICATION NUMBER: US/09/215,076

PRIOR PILITG DATE: 1999-01-20

NUMBER OF SEQ ID NOS: 38054

SOFTWARE: PRESENCE 1993

LENGTHARE: PRESENCE OF WINDOWS VERSION 3.0
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ORGANISM: Homo sapiens
FEATURE:
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
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; NAME/KEY: unsure
; LOCATION: (1)..(697)
; OTHER INFORMATION: n =
US-09-873-319-679
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Best Local Similarity:
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US-09-918-995-11181
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Bublication No. US20030134280A1

GENERAL INFORMATION

GENERAL INFORMATION

TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperplas

TITLE OF INVENTION: Gene Expression Profiles

TITLE OF INVENTION: Gene Expression Profiles

TITLE OF ILLING DATE: 2001-09-24

CURRENT APPLICATION NUMBER: US/09/960,706

CURRENT APPLICATION NUMBER: 60/223,323

PRIOR FILING DATE: 2001-09-24

PRIOR FILING DATE: 2001-06-05

NUMBER OF SEQ ID NOS: 1124

SOFTWARE: Patentin Ver: 2:1

LEASTHARE PATENTING PATE: 2001-06-05

MUMBER OF SEQ ID NOS: 1124

SOFTWARE: Patentin Ver: 2:1

LEASTHA: 697
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                                                                                      63 AAATACGAGAAACGGGTACATTCACCCGGTCAACCTGACGTGGCCCTTTATGGTGGCCGGG 122
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      3 GACACGCTCCAGGCTCCAGCTACATCGCCCACTTGAGGCAGATCCTGGCTAACGAC 62
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                                              139 LysTyrGluAsnGlyTyrIleHisProValAsnLeuThrTrpProPheMetValAlaGly
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ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Genbank Accession No. US20030134280A1 W73859
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Matches:
Conservative:
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LOCATION: (1)..(697)
OTHER INFORMATION: n = a or c or g or
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Sequence 679, Application US/09873319A
Publication No. US20030134324A1
GENERAL INFORMATION:
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APPLICANT: Robison, Keith E.
TITLE OF INVENTION: No. US20020132090Alel Nucleic Acid and Protein Homologs
FILE REFERENCE: S800-119
CURRENT APPLICATION NUMBER: US/09/833,381
CURRENT FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 09/516,448
PRIOR APPLICATION NUMBER: 09/516,448
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 2050
SOFTWARE: FastSEQ for Windows Version 3.0
                                      88 GluargalaargMetargValLeuSerLysAlaPheSerArgLeuLysThrLeuPro 107
                                                                                                                  482
                                                                                                                                                   108 TrpValProFroAspThrLysLeuSerLysLeuAspThrLeuArgLeuAlaSerSerTyr 127
                                                                                                                                                                      483 ACCGAGCCGGACCGCAAGCTCTCCAAGATTGAGACGCTGCGCCTGGCCTCCAGCTAC 542
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                                                                                                                                                                                                                    128 IleAlaHisLeuArgGlnIleLeu 135
                                                                                                                                                                                                                                                                                                                 ; Sequence 505, Application US/09833381
; Patent No. US20020132090A1
; GENERAL INFORMATION:
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TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity:
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APPLICANT: Ji, Darren
APPLICANT: Journal Arelrod, Douglas W.
APPLICANT: Ascard, Meelam
APPLICANT: Gook, Jonathon S.
APPLICANT: Houghton, Adam
APPLICANT: Bistein, Richard
APPLICANT: Houghton, Adam
APPLICANT: Houghton, Adam
APPLICANT: Mertz, Lawrence
TITLE OF INVENTION: Gene Expression Profiles Associated with Osteoblast Differentiati
FILE REFERENCE: 04421-203-W0
CURRENT APPLICATION NUMBER: US 60/255,882
PRIOR APPLICATION NUMBER: US 60/255,882
PRIOR APPLICATION NUMBER: US 60/285,691
PRIOR FILING DATE: 2001-12-18
PRIOR FILING DATE: 2001-14-24
NUMBER OF SEQ ID NOS: 149
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 124
LENGHARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                               243 GAGGACGGGGAAGGGAGAGCTCCGACGAGAAACCCTGCCGTGTGCATGCTGCG 302
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US-10-450-826-124
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Matches:
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180.50
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ORGANISM: Homo sapiens
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Email: bento-soares@uiowa.edu
Tissue Procurement: Mary Hendrix
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/humanfl.html
The following repetitive elements were found in this CDNA
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Normalization and subtraction: two approaches to facilitate gene
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IMAGE:30557534 5', mRNA sequence.
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 Homo sapiens
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RESULT 1
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- MODEL from the p2n.model - DEV=x1h
- MODEL fastap - SUFFIX=rst - MINNATCH=0.1 - LOOPCL=0 - LOOPEXT=0
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Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                  OM protein - nucleic search, using frame_plus_p2n model
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Fgapop 6.0, Fgapext Delop 6.0, Delext
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Ebert, L. Henil, O. Hennig, S., Neubert, P., Partsch, E., Peters, M., Radelof, U., Schneider, D. and Korn, B.
Radelof, U., Schneider, D. and Korn, B.
Human UnigeneSet - RZPD3

AL Upublished (2003)
Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; INAGP998N24234.
RZPD; INAGP998N3679111N0-972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6 D-14059 Berlin, Germany
Tel: 449 30 32639 111
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                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 796)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13r, Primer sequence: TTCACACAGGAACAGCTATGAC.
Location/Qualifers
1. 796
/organism="Homo sapiens"
/mol_type="mRNA"
/db zref="taRNA"
/db zref="taRNA"
/clone="IMAGP998N24234 ; IMAGE:151511"
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  BX107489 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGp998N24234 ; IMAGE:151511, mRNA sequence.
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                                                                   BX107489.1 GI:27834707
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917.00
100.00%
100.00%
                                                                                                           Homo sapiens (human)
Homo sapiens
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                                                                                                                                                                     /tissue type="Chondrosarcoma Lung Metastasis cell lines"
/lab hogie="DH10B (T1 phage resistant)"
/clone lib="NHH MGC_21"
/clone lib="NHH MGC_21"
/note="Organ: Lung; Vector: pXx-Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dr
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with Not I and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is GATAAGGCCA. Tissue was provided by Mary Hendrix."
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sequence: 1-81, > (GA)n#Simple_repeat (matched compliment)
Seg primer: pYX-5.
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                                                                                              organism="Homo sapiens"
                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30557534"
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Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 9100 GE EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
191 910 6 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                              458 AAGGCCCCCCCAAGAAGAGCCCCCTGAGCGGGGTCAGCAGGAGGAGGAAGCAGGTCCAG
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                                                                                         MetSerThrGlySerLeuSerAspValGluAspLeuGlnGluValGluMetLeuGluCys
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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Homo sapiens
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Contact: Genoscope
Genoscope - Centra National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.ons.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and Ecox V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
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ALS50251 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA COT 05-NORMALIZED Homo sapiens CDNA CLONE CSDI0139YJ05 5-PRIME, MRNA sequence.
ALS50251
ALS50251.3 GI:45750628
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                                                                                                                                                                                                                                                                                                                                              GluAsnGlyTyrIleHisProValAsnLeuThrTrpProPheMetValAlaGlyLysPro 160
                                           434
                                                                                  ArgAsnAlaAlaAsnAlaArgGluArgAlaArgMetArgValLeuSerLysAlaPheSer 100
                                                                                                                                                                                                                                                           LeuArgLeuAlaSerSerTyrIleAlaHisLeuArgGlnIleLeuAlaAsnAspLysTyr 140
  80
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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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Li, Mass, Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                   GluSerAspLeuLysGluValValThrAlaSerArgLeuCysGlyThrThrAlaSer 179
                                                                                                                                                                                                   AGACTCAAGACCACCCTGCCCTGGGTGCCCCCCGACACAACAACTCCAAGCTCTCCAAGCTGGACACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            LysAlaProThrLysLysSerProLeuSerGlyValSerGlnGluGlyLysGlnValGln
                                                                                                                                                                   101 ArgleulysThrThrLeuProTrpValProProAspThrLysLeuSerLysLeuAspThr
                                                                                                                                                                                                                                                                                                                                                                                   615 GAGAACGGGTACATTCACCCGGTCAACCTGACGTGGCCCTTTATGGTGGCCGGGAAACCC
                                    AAGGCGCCCACCAAGAAGAGCCCCCTGAGCGGGGTCAGCCAGGAGGGAAGCAGGTCCAG
                                                                                                                            For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODI039CE03QP1&c=3812.f. Location/Qualifiers
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Query Match:
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Pred. No.:
                                         375
61
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Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
Bp 1910 GENYY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
191 910 000 GENYY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
18t strand cDNA was primed with a Not1-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSpORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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CR616308 CR616308.1 GI:50497115
                                                                                                                                                                                                                                                                                                                  Length:
Matches:
                                                                                                                                                              1.1250
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                                                                                                                                                                                sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                         (1-1250)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      440 AAGGCGCCCACCAAGAAGAGCCCCCTGAGCGGGTCAGCCAGGAGGGGGGAGCAGGTCAG 499
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1 (bases 1 to 1250)
1 (bases 1 to 1250)
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Full-length cDNA libraries and normalization
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HTC; CNSLT_CDNA.
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Homo sapiens (human)
Homo sapiens
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2 (bases 1 to 1250)
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/mol_type="mRNA"
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                                                                                                                                                                                                                 BM544256 1038 bp mRNA linear EST 20-FEB-2002
AGENCOURT 6490671 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5587760
5., mRNA Sequence.
BM544256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Profurement: Invitrogen
Tissue Profurement: Invitrogen
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12357 row: m column: 09
High quality sequence stop: 774.
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitogen.
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                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. [Limes 1 to 1552]
Limes, Gruber, C.; Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization
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62 AlebroThity@Lyses-proLemSerglyValSergluGluGluGluVysgluvalges 18 and 20 and 2	Query Match:         99.35%         Indels:         0         .           DB:         1         Gaps:         0         .           US-09-701-674A-23 (1-179)         X AL575799 (1-1024)         .         .           US-09-701-674A-23 (1-179)         X AL575799 (1-1024)         .         .           QY         1	91 ArghenalahaanalaargdluhrgalaargwalleuSerLysalaaPheSer 100 736 CGCAACGCCGCCAACGCGCGAGGCCCCCATGCGATGCTGAGGCCTTCTCC 677 679 101 ArgleuLysThrThrLeuProTrpValProProAspThrLysLeuSerLysLeuBpThr 120 879 121 LeubrgLeuAlaSerSerTyrIleAlaHisLeubrgGAGCCTCCCAAGCTCTCCAAGCTCCAAGCTGGACAG 870 AAACTCAAGACCACCTGCCTGGGTGCCCCGGAACCTCCAAGCTGGACAG 871 LeubrgLeuAlaSerSerTyrIleAlaHisLeubrgGInIleLeublaAshaSpLysTyr 140 870 L121 LeubrgCGGTCCAGCTGCCTGGGTGCCCCAAGCTCCAAGCTGGACAG 871 LeubrgCGGTCCAGCTGCCTGGGTGCCCCAAGCTCCAAGCTGGACAG 872 CTCAAGCTGGCTCCAGCTGCCCCACTTGAGGCAGATCCTGGCTAACGACAAATAC 557 873 GAGAACGGGTCCAGCTCAACGTGGCCCTTTATGGTGGCCGGGAAACC 497 874 GAGAGGGTAACTCACCCGGTCAACGTGGCCCTTTATGGTGGCCGGGAAACC 497 875 GAGAACGGGTCAACTCACCCGGTCAACGTGGCCCTTTATGGTGGCCGGGAAACC 497 876 GAGAGTGAACTGACCTGAACGTGGCCCTTTATGGTGGCCGGGAAACC 497 877 GAGAGTGAACTGAACGTGGCCGCTTTATGGTGGAACCC 497 878 GAGAGTGAACTGACCGCGCGAGCCGCTTTATGGTGGAACCCCCTTAATGTGGGAACCC 497 879 GAGAGTGAACTGACCGCGCGAGCCGCTTTATGTGGGAACCC 497	AL552119 AL552119 TO SAPERING SERVING	For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODIO59CD09QP1&c=3812.f. Location/Qualifiers 1.099 11099 11099 /organism="Homo sapiens"
	81 321 101 381 121 141 141 161	615 6-APR-2004 oiens cDNA leostomi;		1024 177 0
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/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime and enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene discovery
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CF127519.1 GI:33205841
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910.00
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Best Local Similarity:
Query Match:
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/urganism="Homo sapiens"
/mol type="mRNA"
/mol type="mRNA"
/db_xref="texon:9666"
/clone="InMagE:305663"
/clone="InMagE:305663"
/lab_bost="Publio" (Tiphage resistant)"
/clone lib="Not II" (The library was constructed according Site_2" (Denou and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand CDNA synthesis was primed with Oligo-dT primer containing a Not I site. Double strand CDNA was size fraction, ligated with RosR I adaptor, digested with Not I and then cloned directionally into pXX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is GATAAGGCCA. Tissue was provided by Mary Hendrix."
                                                                                                                                  University of Iowa 135 Grad Also MEBRF, Iowa City, IA 5242, USA 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA 7E1: 319 315 956 MEBRF, Iowa City, IA 52242, USA 7E1: 319 315 956 Memal: bento-soares@uiowa.edu Tissue Prourement: Mary Hendrix CDNA Library preparation: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/humanfl.html
The following repetitive elements were found in this cDNA sequence: 172-253, > (GA) #Sumple_repeat (matched compliment) Seq primer: pYX-5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    317
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Coordinated Laboratory
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BM923344 10-WAR-2002 AGENCOURT 6626079 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5758942 5', mRNA sequence.
BM923344
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
I (bases I to 1098)
III MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: Gapbbs-remail.cih-gov

Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM12803 row: i column: 23
High quality sequence stop: 693.
.92 ATGTCCACCGGCTCCCTCAGCGATGTGGAGGACCTTCAAGAGGTGGAGATGCTGGACTGC
                                                                             41 SerSerAsnCysGluAsnGlySerProGlnLysGlyArgGlyGlyLeuGlyLysArgArg
                                                                                                                                                                                                                 312 AGCTCCAACTGCGTGACCGGCTCTCCCCAGAAGGGCCGCGGCGGCGGCTGGGCAAGAAGAGG
                                                                                                                                                                                                                                                                             61 LysAlaProThrLysLysSerProLeuSerGlyValSerGlnGluGlyLysGlnValGln
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                                                              121 LeuargieualaSerSerTyrIlealaHisLeuargGlnIleLeualaAsnAspLysTyr 140
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           558 AGACTCAAGACCACCCTGCCCTGGGTGCCCCCGGACACCAAGCTCTCCAAGCTGGACACG 617
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Fax: 33 (0) 5.61.28.53.08
Faxil: toosese@tooulouse.ina.fr
Sequence cleaned of vector, adaptator and repetitions. Contact us at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
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Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
1 (bases 1 to 827)
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Institut National de la Recherche Agronomique
Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan
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                                                                                                                                                                                                                                                                                      827 bp mRNA linear EST 0
BX926295 Sus Scrofa library (scan) Sus scrofa cDNA clone
scan0021d.a.24 5prim, mRNA sequence.
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Location/Qualifiers
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BX337699.2 GI:46283026
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stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EocNv site i destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH MGC Library.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae,
Li, Wase, Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
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178
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Matches:
Conservative:
Mismatches:
Indels:
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901.00
99.44%
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Homo sapiens
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Best Local Similarity:
Query Match:
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VERSION
KEYWORDS
SOURCE
ORGANISM
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Pred. No.:
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TITLE
JOURNAL
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BX337699
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: sequence@senoscope.cns.fr, Web.
Is trand cDN was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-grand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol type="mcNA"
/db xref="raxon:5606"
/clone="CSODIO48YEL5"
/clone="CSODIO48YEL5"
/clone lib="PtACENTA COT 25-NORWALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORWALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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Mammalia, Butheria; Rocentia; Sciurogiacul; Fullians; Fullians; Autheria; Rocentia; Sciurogiacul; Fullians; Fullians
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BY710826
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The Institute of Physical and Chemical Research (RIKEN)
T-22 Suehiro-ho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-922
Fax: 81-45-503-9216
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Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Horl,F.,
Irohani,K., Ishi,Y., Itoh,M., Kagawa,T., Kawai,J., Kojima,Y.,
Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N.,
Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
                                                                                                                                                                                     141 GluAsnGlyTyrIleHisProValAsnLeuThrTrpProPheMetValAlaGlyLysPro 160
                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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669 AGACTCAAGACCACCTGCCTGGTG-CCCCCGACACCTCTCCAAGCTGGACACG
                                                            LeuArgLeuAlaSerSerTyrIleAlaHisLeuArgGlnIleLeuAlaAsnAspLysTyr
                                                                                                    Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
Mus musculus
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BY710826
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Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BRail: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
          EST 06-APR-2004
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          AL574170 ALCO SADIENS PLACENTA COT 25-NORMALIZED Homo SADIENS CDNA CODE CSODI039YJ05 3-PRIME, MRNA SEQUENCE.
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(bases 1 to 1085)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /Lissue type="PLACENTA COT 25-NORMALIZED"
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/note="lst strand cDNA was primed with a Not1-Oijgo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODI039CE03NP1&c=3812.f. Location/Qualifiers
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890.00
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            Direct Submission

Computational Analysis of Full-Length Mouse CDNAs Compared with Human Genome Sequence Same. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                  prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
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Matches:
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
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/db_xref="taxon:10090"
/clone="2610027010"
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AAGGCGCCCACTAAGAAAGCCCCGCTCAGCGGGGTCAGCCAGGAGGGCAAGCAGGTCCAG 480
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learch completed: December 17, 2004, 00:03:53 ob time : 2876 secs

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Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage:
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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HTC; CNSLT_CDNA.
HTC; CNSLT_CDNA.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
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http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
   CF128914
CF1278998
CF1378998
CF1364905
CF126467
BM8111952
CN409630
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/plasmid="pCMVSPORT_6"
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.larity 100.0%; Pred. No. 1.2e-287;
Conservative 0; Mismatches 0; Indels
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/db_xref="taxon:9606"
/clone="CSODIO70YK16"
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TITLE
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CR616308
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CF127514 WI-HF-ETO
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(c) 1993 - 2004 Compugen Ltd.
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1141 GTAGATCATAGGATAGCTGACTTTGACAGTCACATTTATAAAGTAATTCACTTAAAGATA 1200 1145 GTAGATCATAGGATAGCTGACTTTGACAGTCACATTTATAAAGTAATTCACTTAAAGATA 1204 1201 TATATTTTTTCAAACAAGTTTTGCTACTTTGAAAATAAAT	157 CR606057 TION full-length cDNA clone CS0DI039YJ05 of Placenta Cot 25-normalized of Homo sapiens (human). ILON CR606057 TON CR606057.1 GT:50486864				S	/organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="CSODIO39YJ05"		Query Match 97.5%; Score 1240; DB 3; Length 1250; Best Local Similarity 100.0%; Pred. No. 1e-285; Matches 1240; Conservative 0; Mismatches 0; Indels 0; Gaps 0	1 TCTACGGCCACCACTCTGGGAQATGGGGAAACAGAGGGCCGGTTCCTCTGCTGCAGAAGTC 60	61 CTCGGGGTTCCTTCTCACACTCTGCGAAGGGGAAAGGGTTGTGAGACCCAACACACAC	121 CAACTCCAGCTCCCAGCAGGAGGTGCTGCGCACACTCGGGAGGCCTCTTGGTTTCAGG 180	181 GRETCTCTGTCTCTCTCACCCTGTTCCTCGTCTTCTCTGTCTCTGTCTCTCTC	241 CTCTCTCCCTCGTCCACCTCCCCAAACATGTCCACCGCCTCCCTC
8 8 8 8	RESULT 2 CR606057 LOCUS DEFINITION ACCESSION VERSION	KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE	JOURNAL REMARK REFERENCE AUTHORS	COMMENT	FEATURE	i	ORIGIN	Quer Best Matc	S S	8 &	\$ 8 8	\$ g	8 %
61 CTCGGGGTTCCTTCTCACAACTCTGCGAAGGGGAAAGGGTTGTGAGACCCAACCAGACCC 120	8 8 5 4 4 1 4 5	CTTC   CTTC   CTTC   CTTC   CTTC   CTTC   CTCA   CT		485 GTCAGGAGGGGAAGGCCCAACGCCCAACGCGCAACGCGGGGAAGGGGGG	601 GACACCAAGCTCTCCAAGCTGGACACGCTCAGGCTGGCGTCCAGCTACATCGCCCACTTG 660	661 AGGCAGATCCTGGCTAACGACAATACGAGAACGGGTACATTCACCCGGTCAACCTGACG 720	721 TGGCCCTTTATGGTGGCCGGGAAACCCGAGAGTGACCTGAAAGAAGTGGTGACCGCGAGC 780 125 TGGCCCTTTATGGTGGCCGGGAAACCCGAGAGTGACCTGAAAGAAGTGGTGACCGCGAGC 784	781 GGCTTATGTGGAACCACCGGGTCCTGACCTTGGAGGTGCGAGTCTGGGAAAAGGGGGGCTC 840 	841 CCGGGGGGAGCGGCCCCGGAAGGCGACCCCTGCCCTCAGTGCTTCTGTTTC 900	4 N	1 ATTCGTTTCCAAACCAG 	1021 TATTAACTTCTACCGTGAATGACTCTGCAAGCCTTGCTGGAGGTGCAATATGTAATT 1080 	1 ATAATATATAAATAGATAAGAGCCCTATCAATGTATCTTT 

SOURCE ORGANISM Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Ver Mammalia; Butheria; Primates; Catarrhini; H REFERENCE 1 (bases 1 to 1221) AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D TITLE Full-length cDNA libraries and normalization JOURNAL Unpublished REMARK Contact: Feng Liang Email: fliang@lifetecl http://fulllength.invitrogen.com/ InvitroGen REFERENCE 2 (bases 1 to 1221) AUTHORS Genoscope. TITLE JOURNAL Submission JOURNAL Submitted (20-JUL-2004) Genoscope - Centre 1	BP 191 91006 EYRY cedex - FRANCE (E-mail : 1- Web : www.genoscope.cns.fr)  COMMENT 1st strand cDNA was primed with a NotI-oligg end enriched, double-strand cDNA was digest into the Not I and EcoR V sites of the pCMV was normalized. Library was constructed by idivision of Invitrogen.  FEATURES : Location/Qualifiers   Location/Qua	/clone="CSULUSYIHI"" /tlasmid="pcMVSPORT_6"  ORIGIN Query Match 96.0%; Score 1221; DB 3; L6 Best Local Similarity 100.0%; Pred. No. 3.6e-281; Matches 1221; Conservative 0; Mismatches 0;	GGGGGGAAA(GGGGAAA) GGGAGTGGGGAAA CAACTCTGCGAAGG	Qy         129 GCTCCCAGGAGGTGGCTGGCCCACACTCGGGAGGCCTC	Qy         249 CTCGTCCACTCCCCCAAACATGTCCACCGGCTCCCTCAGCG	369	0y 429 cggccTgggCaAgaGaGaCaCaCaAgaAgaGCCCACAGAGAGAGCCCACAGAGAGAGACCCACAGAGAGAGCCCACAGAGAGAGCCCACAGAGAGAGCCCACAGAGAGAGCCCACAGAGAGAGCCCACAGAGAGAGCCCACAGAGAGAGCCCACAGAGAGAGCCAG
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division of Invitrogen. This sequence belongs to sequence 3812 f. For more information about this cluster, see http://www.genoscope.ons.fr/cdna?s=CSODI039CE03NP1&c=3812. Location/Qualifiers
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Bmail: seqrefégenoscope.cns fr. Web : www.genoscope.cns.fr
Email: seqrefégenoscope.cns fr. Web : www.genoscope.cns.fr
end charand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001)
On Feb 16, 2001 this sequence version replaced gi:31295505.
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BP 191 91006 EVRY cedex - France
Email: seqrefe@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a Noti-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a adivision of Invitrogen. This sequence belongs to sequence cluster
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                                                                                  TACTTACAAAGATTCCCATCTATTAACTTTAACTTCTACCGTGAATGACTCTGCAA 1050
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AL552119 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DIOS9YH17 5-PRIME, mRNA sequence.
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/mol_type="mRNA"
/db_xref="taxon:050"
/clone="CSOUGSY9H17"
/tissue_type="PLACENTA COT 25-NORMALIZED"
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primer. Five prime end enriched, double-strand cDNA was
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized.
                                KACTTACAAAGATTCCCATCTATTTAACTTTAATAACTTCTACCGTGAATGACTCKGCAA
                                                                                                                                                   GCCTTGCTGGTCCAAGTGCAATATGTAATTATAAATATAAATAGAGGCCTATCA
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              CCCGCGAGACACTTTACAACGAGGAGAGTTCGTTTCCAAACCAGAGGAGATCAATTG
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Contact: Genoscope
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Catarrhini; Hominidae;
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (human)
Homo sapiens
Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Primates;
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Best Local Similarity 96.8*
Matches 1050; Conservative
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AUTHORS
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AL552119
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KEYWORDS
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Contact: Genoscope Genoscope Genoscope Genoscope - Centra National de Sequencage Genoscope - Centra National de Sequencage BP 191 91006 EVRY cedex - France BP 191 91006 EVRY cedex - France BP 191 sequencage cns.fr. Web: www.genoscope.cns.fr est end cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECOR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a 3812.f.
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AL550251 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
clone CSODI039YJ05 5-PRIME, mRNA sequence.
AL550251
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
664 ACCCTGCCCTGGGTGCCCCCCCGACACCTCTCCCAAGCTGGACACGCTCAAGCTGGCG
                                                    TCCAGCTACATCGCCCACTTGAGGCAGATCCTGGCTAACGACAAATACGAGAACGGGTAC
                                                                                       ATTCACCCGGTCAACCTGACGTGGCCCTTTATGGTGGCCGGGAAACCCCGAGAGTGACCTG
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hor
1. (bases 1 to 1024)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                                                       AL575799 nRNA AL575799 Homo sapiens PLACENTA COT 25-NORM clone CSODIO70YK16 3-PRIME, mRNA sequence.
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/db_xref="taxon:9606"
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QY         841 CCGGGGGGCGGGCCCGGGAAGGCAACCCTGCCTCTGTCTCTGTTCTGTTC         900           Db         851 CCGGGGGGCCCGGGAAGGCGAACCCTGCCCTCAGTGCTCTCTGTTCTGCTTC         910           QY         901 CCCCTCGCAATGCTCCTCTTCTGTCCCACCCGGGAGAACACTTTACAACGACGAGGAG         960           Db         911 CCCCTCGCAATGCTCCTCTTCTTGTCCCACCCGGGAGAACACTTTACAAGACGAGGAG         960           QY         961 ATTCGTTTCCAAACCAGAGGAACACTTACAAAGATTCCCATCTTTACAAGATTAACTT         1020           Db         970 ATTCGTTT-CAAACCAGAGGAACATTTTTTACAAAATTCCCATCTATTAAATT         1020           QY         1021 T         1021	Db   1026 W 1026   1026   1026   1026   1026   1026   1026   1026   1020   10	N R N	Contact: Genoscope Genoscope - Centre National de Sequencage Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France BP 191 91006 EVRY cedex - France Ist strand cDNA was primed with a NotL-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster	ttp://ww	Purlaner. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."  Query Match  Query Match  Pest Local Similarity 75.5%; Score 959.8; DB 1; Length 1169;  Best Local Similarity 97.3%; Pred. No. 1.2e-218;  Matches 988; Conservative 4; Mismatches 21; Indels 2; Gaps 2;  Oy 207 TCCTGGCTTTCTGTCTCTGTCTCTCTCTCTCTCTCTCTC
cyanism="Homo sapiens"  ol_type="mRNA"  ol_type="mRNA"  b_xref="taxon:966"  b_xref="taxon:9666"  lone="CSODI039405"  lone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"  lone lib="Homo sapiens"  lone cot the pCMVSPORT for the Normal sapiens of the pCMVSPORT for the Normal sapiens in the Normal sapi	Ouery Match Ouery Match Ouery Match Best Local Similarity 7:9%; Pred. No. 1.3e-219; Matches 1000; Conservative 7; Mismatches 9; Indels 5; Gaps 3;  Matches 1100; Conservative 7; Mismatches 9; Indels 5; Gaps 3;  Qy	121   CAACTCCAGCTCCCAGCAGAGGGTGGCCACTCGGGAGGCCTCTTGGTTTCAGG 180   131   CAACTCCAGCTCCCAGCAGGGCCTCCTGGTTTCAGG 180   131   CAACTCCAGCTCCCAGCAGGGCCTCCCCACCACCACCACCACCACCACCACCACCACCACC	Db   251   CTCTCTCCTCGCCCCCCCCCCCCCCCCCCCCCCCCCC	431 GGCGGGGGGGCTGGGCAAGAGGACGCCCACCAAGAAGAGCCCCTGAAGGGGGGGG	S51 AIGCGAGTGCTGAGCCTTCTCCAGGCTGAGCCCTGCCTGGGTGCCCCCC

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)	387 GAGCTCCAACTGCGAGAATGGGTCTCCCCAGAAGGGCGGGGGGGG	GAAGGGGCCCACCAAGAAGAGCCCCCTGAGGGGGGGTCAGCCAGGAGGGGAAGCAGGTCCAGAAGGCCCCTGAGCGGGGGTCAAGCAGGAAGGA	GCGCAACGCCGCCAACGCGCGAGAGCGGGCCCGCATGCGAGGTGCTGAGCAAGGCCTTCTC	720 GCGCAACGCCGCCAACGCGCGAGAGCGGGCCCGCAIGCGAGIGCIGAGCAAGGCCTICTC	GCTCAGGCTGGCGCTCCAGCTACCACCTTGAGGCAGATCCTGGCTAACGACAAAAA	CAGAACGGGTACATTCACCCGGTCAACCTGACGTGGCCCTTTATGGTGGCCGGGAAACCCCGAGAACGGGTAACGCGGGAAACCCGAGAACGCCTTTATGGTGGCCCGGGGAAACC	747 CGAGAGTGACCTGAAAGAAGTGGTGACCGCGAGCGGCTTATGTGGAACCACGGGTCCTG 806	ACCTTGGAGGTGCGAGTCTGGGAAAGGCGCGCTCCCGGGGGAGCGGGCCCCGGGAAGGC	ACCITICAGE CONTRACTOR	361 GACCCCTGCCTCAGTGCTCTGTGTTCTGCTTCCGCTCGCAATGCTCCTCTCTCT	301 CCACCCCGCGAGAACACTITACAACGACGAGGAGATICGTTTCCAAACCAGAGGAGATCA 242 987 attictactitacaacaacaacaccaactitataactitaaactitaactitaacaacaacaacaacaacaacaacaacaacaacaacaac	ALIGENCIA PARAGETICA CONTINUE IN INTERNACIA DE LA CARRACTICA CONTINUE IN INTERNACIA DE LA CARRACTICA CONTINUE INTERNACIA DE LA CARRACTICA DEL CARRACTICA DE LA CARRACTICA DE LA CARRACTICA DEL CARRACTICA DE LA CARRACTICA DEL CARRACTICA DEL CARRACTICA DE LA CARRACTICA DEL CAR	1047 GCAAGCCTTGCTGGTCCAAGTGCAATATGTAATTATAAATAGAATAAGAGGCCT 1106 	ATCAATGTATCTTTTGTACAATATGTTGTAAAATGTAGATCATAGGATAGGATGCTTTGA	AICHAIGIACHTATAAAGTAATATGATAAATATATATATTTTTTCAAAGAAGTT 1221	61 CAGTCACATTTATAAAGTAATTCACTTAAAGATATATATA	RESULT 9	AL552380 LOCUS AL552380 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA	clone CSODI070YK16 5-PRIME, mRNA sequence. ACCESSION AL552380		NISM	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 965)
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- Centre National de Sequencage

OG EVRY cedex - France

Iref@genoscope.cns.fr, Web : www.genoscope.cns.fr

cDNA was primed with a NotI-oligo(dT) primer. Five prime

acd, double-strand cDNA was digested with Not I and cloned

Not I and EcoR V sites of the pCMVSPORT 6 vector. Library

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of Invitrogen. This sequence belongs to sequence cluster
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/chote="ist strand cDNA was primed with a NotI-oligo(dT)
/chote="ist strand cDNA was primed into the Not I and BcoR V
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Pred. No. 1.1e-213;
0; Mismatches 0;
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Query Match         73.2%;         Score 931;         DB 5;         Length 1056;           Best Local Similarity         96.9%;         Pred. No. 9.2e-212;         Pred. Similarity         96.9%;         Pred. No. 9.2e-212;         Pred. Similarity         2;         Gaps         2;           Qy         1	CAACTCCAGCTCCCAGCAGAAGATGGCTGCGCACACTCGGGAGGCCTCTTGGTTTCAGG	241 CTCTCTCCCTCGTCCACTCCCCCAAACATGTCCACCGGCTCCCTCAGCGATGTGGAGGAC 300		Oy         541 ATGCGAGTGCTGAGGCTTCTCCAGACTCAAGACCACCTGCCCTGGGTGCCCCC         600           bb         551 ATGCGAGTGAGCAAGGCTTCTCCAGACTCACCCTGCCCTGGCCTCCCC         610           col         GACACCAAGTTCTCCAAGCTTCTCCAGGTTCCAGCTCCAGCTCCAGCTCCACCTTG         600           col         GACACCAGTTCTCCAAGCTTCAAGCTCCAGCTCCAGCTACATTCGCCCACTTG         600           col         GACACCAGTTCTCCAAGCTCAAGCTCAGCTCCAGCTACATTCACCCAGCTTG         600           col         GAGCAGATCTTCCAAGCTCAAAAAACCAGAAACGGGTACATTCACCCAGCTCAACCTTG         670           col         GAGCAGATCCTGGCTAAAAAAAAAAAAAAAAAAAAAAAA	0.5   0.5
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AGENCOURT 6626079 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5758942
5', mRNA sequence.
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                                   380 GACTCAAGACCACCCCGCCCCGGACACCAAGCTCTCCAAGCTGGACACGC
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/clone_lole_niny_MQC_125"
/note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;
Site_l: EcoRV (destroyed); Site_2: Not1; RNA source pool of three ovaries, from females ranging in age from 38 to of three ovaries, from females ranging in age from 38 to de took of the primed and directionally cloned (BCoRV site is destroyed upon cloning). Average insert size 2.1 kb, insert size range 1-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 036."
1038 bp mRNA linear EST 20-FEB-2002
AGENCOUST 6490671 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5587760
5', mRNA sequence.
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NH-WGC http://mgc.ndi.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12357 row: m column: 09
High quality sequence stop: 774.
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Pred. No. 2.9e-199;
0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .1038
/organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
/clone="MAGE:5587760"
/lab_host="DH10B"
                                                                                                                                         BM544256.1 GI:18775358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69.1%;
ilarity 98.9%;
Conservative
                                                                                                                                                                                          Homo sapiens (human)
Homo sapiens
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Best Local Similarity
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                                                              DEFINITION
                                                                                                                                                                                                                     ORGANISM
                                                                                                              ACCESSION
VERSION
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748 559 808 619 868

499

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E LOGES L. (10.79). Hennig, S., Neubert, P., Partsch, E., Peters, M., Radelof, U., Schneider, D. and Korn, B.

Radelof, U., Schneider, D. and Korn, B.

Human Unigenest - RZPD3

AL Duublished (2003)

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

RZPDIIB; I.M.A.G.E. cDNA Clone Collection,

Human Unigeneset - RZPD3 (RZPDLIB No.972)

http://www.rzpd.de/CloneCards/Cgi-
bin/showlib.pl.cgi/response?libNo-972 Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Heubnerweg 6, D-14059 Berlin, Germany

Fax: +49 30 32639 111

www.rzpd.de
                                                                                                                                                                                                                       BX107489 To Arba 1inear EST 06-FEB-2003 BX107489 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGP9998N24234 ; IMAGE:151511, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTyT3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 796)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        primer:
        134 CAGCAGAAGTGGCTGCGCCACTCGGAAGGCCTCTTGGTTTCAGGGTCTCTCTGTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74 CTCACAACTCTGCGAAGGGGAAAGGGTTGTGAGACCCAACCAGACCCCAACTCCAGCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free from RZPD; contact RZPD (clone@rzpd.de) for further information. Seq M13r, Primer sequence: TTTCACACAGGAAACAGCTATGAC. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. 796
/organism="Homo sapiens"
/mol type="mRNA"
/db xrse="taxon:9606"
/clone="IMAG9998N24234 ; IMAGE:151511"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62.5%; Score 795; DB 5; Le
llarity 100.0%; Pred. No. 3.2e-179;
Conservative 0; Mismatches 0;
                                                                                   853 GGCCCCGGGAAGGCGACCCC 872
                                                                                                                        854 GGGCCCGGGAAGGCGCACC 873
                                                                                                                                                                                                                                                                                                    BX107489.1 GI:27834707
                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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795;
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BX107489
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                                   /lab_host="DHIUGE"
/clone lib="MHH MGC 116"
/note="Organ: pooled colon, kidney, stomach; Vector:
pCMV-SPORT6; Site 1: Not1; Site 2: EccRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EccRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
fruber (Invitrogen). Research Genetics tracking code
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGATGTTGGAATGTGACGGCTTGAAATGGATTCGAACAAGGAATTTGTGACTTCCAACG 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGAGCACCGAGGAGGCTCCCAACTGCGAGAATGGGTCTCCCCAGAAGGGCCGGCGCGGCC 433
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                                                                                                                                                                                                                                                                                                                                                                                                                                       14 CTCTGGGGAGAGGGGGAAACAGAGAGCGGTTCCTCTGCTGCAGAAGTCCTCGGGGGTTCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAGCAGGAGGTGGCTGCCCCACACTCGGGAGGCCTCTTGGTTTCAGGGTCTCTCTGTCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGAAGCAGGTCCAGCGCAACGCCGAACGCGCGAGAGCGGGCCCGCATGCGAGTGCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGAAGCAGGTCCAGCGCAACGCCCCAACGCGCGAGGCGGGCCCGCATGCGAGTGCTGA
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                                                                                                                                                                                                                                                                                                                                        Length 1098;
                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                   Score 824; DB 4; L
Pred. No. 3.8e-186;
0; Mismatches 15;
/db_xref="taxon:9606"
/clone="IMAGE:5758942"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                   64.8%;
98.1%;
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end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR vs sites of the pCWVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster.  3812.f.  FEATURES  Location/Qualifiers  Location/Qualifi	ORIGIN  Query Match  Best Local Similarity 97.3%; Score 788; DB 5; Length 996;  Best Local Similarity 97.3%; Pred. No. 1.6e-177;  Matches 806; Conservative 5; Mismatches 16; Indels 1; Gaps 1;  Acceptagaganacaga	181	496 496 481 555 616 601 676
61 CAGCAGGAGGCTGCCACACTCGGGAGGCCTCTTGGTTTCAGGGTCTCTCTGTCTC  194 TCTCTCACCCTCTTCCTCGCTTTCTCTGTCTCTCTCTCTC	AGAGGG AGAGGG AGAGGG AGAGGG AGAGGG AGAGGGG AGAGGGGGG	Qy         734 TGGCCGGGAAACCCGAAGTGACCTGAAAGAGTGGTGACCGCGAGCCGCTTATGTGGAA 793           Db         661 TGGCCGGGAAACCCGAGAGTGACCTGAAAGAGTGGTGACCGCAGCCGTTATGTGGAA 720           Qy         794 CCACCGGGAACCCTTGAGTGACCTTGGAAGTGGTCACGCGAGCGGGGGGGG	CLODE CSUDIO6/YOLB 5-FRIME, MKNA Sequence.  RX360244 C G1:46553101  KEYWORDS EST.  SOURCE Homo sapiens (human) ORCANISM Homo sapiens (human) Homo sapiens ENKARYOCA: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Enkaryoca; Metazoa; Chordata; Catarrhini; Hominidae; Homo.  REFERENCE 1 (bases 1 to 996) AUTHORS Li, M.B., Gruber, C., Jessee, J. and Polayes, D.  TITLE Full-length cDNA libraries and normalization JOURNAL Unpublished (2001) COMMENT Genoscope Genoscope - Centre National de Sequencage Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: Segref@genoscope.cns.fr Email: segref@genoscope.cns.fr Ist strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

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Contact: Soares, MB
Contact of Lowa
University of Lowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 310 
                                                                                                                                                                                                                                   CF127519 800 bp mRNA linear EST 05-AUG-2003
UI-HF-ET0-awh-f-14-0-UI.rl NIH MGC_214 Homo sapiens cDNA clone
IMAGE:30554533 5', mRNA sequence.
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Bonaldo, M. F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
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APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
STREET: 3174 PORTER DRIVE
STREET: CALIFORNIA
COUNTRY: USA
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CLASSIFICATION:
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER:
REGISTRATION NUMBER:
REGISTRATION NUMBER:
NAME: Zeller, Karen J.
            PCT - US95-05741-1

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REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 655-0555
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GENERAL INFORMATION:
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-99-227-14
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US-08-552-142A-1
US-08-910-973-1
                                                                                                                                                                                                                                                                                                                                         824507 seqs, 355394441 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                     BLOSUM62
Xgapop 10.0, Xgapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
Delop 6.0, Delext
                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length DB
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112275
112275
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11560
22502
22089
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                                                                                                                                                                     Title:
Perfect score:
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1459 ACGCAGCGGGTCATGGCCAACGTGCGGGAGCGCCAGGGGGCGCCCAGCCGTCGCTGAACGAGGCG 1518
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                         59 ArgArgLysAlaProThrLysLysSerProLeuSerGlyValSerGlnGluGlyLysGln
                                                                                                               -TCTTACGAGGAGCTGCAG
                                                                                                                                                                                            79 ValGinArgAsnAlaAlaAsnAlaArgGluArgAlaArgMetArgValLeuSerLysAla
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APPLICANT: Weintraub, Harold M.
APPLICANT: Weintraub, Harold M.
APPLICANT: Tapscott, Stephen J.
APPLICANT: Tapscott, Stephen J.
APPLICANT: Hollenberg, Stanley M.
APPLICANT: and Proteins
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSES: Christensen O'Comor Johnson KindnessPLLC
STREET: 1420 Fifth Avenue, Suite 2800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Elem PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NATA:
APPLICATION NATA:
APPLICATION NATE: 02-NOV-1995
CLASSIFICATION DATA:
APPLICATION NAMER: US 08/239,238
FILING DATE: 06-MAY-1994
FILING DATE: 06-MAY-1994
FILING DATE: 06-MAY-1994
FILING DATE: 08-MAY-1994
FILING DATE: 08-MAY-1995
ATTORING DATE: 08-MAY-1994
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REFERENCE/DOCKET NUMBER: FHCR-1-8933
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-682-8100
TELEFAX: 206-70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-552-142A-3
; Sequence 3, Application US/08552142A
; Patent No. 5695995
                                                                                                               1423 GGCGGCGGAGTCCGCAG--
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
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STATE: WA
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Factor No. 6756200

GENERAL INFORMATION:
FAPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
APPLICANT: SUKUMAR, Sazaswati
APPLICANT: BYRON, Bilas
APPLICANT: BYRON, Bilas
APPLICANT: DAVIDSON, Nancy
TITLE OF INVENTION: ABERRANTLY METHYLATED GENES AS MARKERS OF BREAST MALIGNANCY
FILE REFERENCE: JULIGATION NUMBER: US/09/771,357
CURRENT APPLICATION NUMBER: US/09/771,357
CURRENT FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 110
SOFTWARR: PALENTIN VERSION 3:0
SOFTWARR: Datentin Version 3:0
FEMCINE 1005
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Matches:
Conservative:
Mismatches:
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Matches:
Conservative:
Mismatches:
Indels:
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Gaps:
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164.00
52.85%
34.96%
17.88%
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 102
SEQUENCE CHARACTERISTICS:
ENGTH: 240 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: KIDNNOTOS
CLONE: 954226
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353.00
93.83*
93.83*
38.50*
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Best Local Similarity:
Query Match:
DB:
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Best Local Similarity:
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89 gAlaArgMetArgValLeuSerLysAlaPheSerArgLeuLysThrThrLeuProTrpVa 109
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67
25
64
43
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                         NAME: Sheines, Diana K.
REGISTRATION NUMBER: 35,356
REFERENCE/DOCKET NUMBER: FHCR-1-10958
TELECOMONICATION INFORMATION:
TELEPHONE: 206-682-8100; 206-224-0735 (direct)
TELEPHONE: 205-6779
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                   FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/239,238
FILING DATE: 06-MAY-1994
PRIOR APPLICATION NUMBER: WO PCT/US95/05741
APPLICATION NUMBER: WO PCT/US95/05741
FILING DATE: 08-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/17532
FILING DATE: 30-October:1996
ATTORNEY/AGENT INFORMATION:
NAME: Sheiness, Diana K.
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                                   CCMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS CURFARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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154.00
46.46%
33.84%
16.79%
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STRANDEDNESS: double
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                                                                                                                                          FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
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DB:
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Patent No. 5795723

GENERAL INFORMATION:
APPLICANT: Tapscott, Stephen J.
APPLICANT: Olson, James M.
TITLE OF INVENTION: Expression of Neurogenic bHLH Genes in Primitive Neuroectoder NURRENCE ADDRESS: 24
CORRESPONDENCE ADDRESS: 24
ADDRESSEE: Christensen O'Connor Johnson KindnessPLLC
                                                                                                                                                                                                                                                                                                                                                                                                                                            181 CACAATGGAGAGGA-GAACGAGGAAGAGTGAAGGGGGATGAGGGAGGAGGAGGACGATGA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    300 GACGAAAGCCCGGGTGGAGCGATTTAAAGTGAGACGCATGAAGGCAAACGCCAGGGAGAG 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            480 GGCTCTTTCTGAGATTTTTAAGGTCCGGCAAAAGCCCCAGACCTGGTGCTTGTACAAAC 539
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                                                                                                                                                                                                                                                                                                                                       5 SerLeuSerAspValGluAspLeuGlnGluValGluMetLeuGluCysAspGlyLeuLys 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45 GluAsnGlySerProGlnLysGlyArgGly------GlyLeuGlyLysArg---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147 oVal-----AsnieuThrTrpProPhe-----MetValAlaGly------Ly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 uSerGlyValSerGlnGluGlyLysGlnValGlnArgAsnAlaAlaArgGluAr
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                                                                                                                                                                                                                                                                                                                                                                             103 AGTICTCAGGATGAAACGATCTGGAGAAA---------
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                                                                                                                                                         1275
67
25
64
43
8
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                              Gaps:
                                                                                                                                                           3.64e-09
154.00
46.46%
33.84%
16.79%
  ORIGINAL SOURCE:
ORGANISM: Xenopus laevis
                                                          CDS
25..1083
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CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101-2347
                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
                                                        , NAME/KEY:
, LOCATION:
US-08-552-142A-3
                                                                                                                                          Alignment Scores
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Alignment Scores: Pred. No.: Score: Score: Score: 154.00 Matches: 67 Matches: 67 Percent Similarity: 16.46 Conservative: 25 Best Local Similarity: 16.794 Mismatches: 43 Mismatches: 64 Query Match: 16.794 Indels: 8 US-09-701-674A-23 (1-179) x US-09-499-227-3 (1-1275) Qy 5 SerLeuSerAspValGluAspLeuGluGluWetLeuGluCysAspGlyLeuLys 24	45 GlubanGlySerProGlnLysGlyAragly  45 GlubanGlySerProGlnLysGlyAragly  45 GlubanGlySerProGlnLysGlyAragly  46 GlubanGlySerProGlnLysGlyAragly  50 GlobanGlyAserProGlnLysGlyAragly  51 AGATGATGAAGAA-AhGAAAAAAT  52 AGATGATGATGATGATGATGATGAGGGATGAAGGAAAAAGAAAAAT  53 GGATGATGATGATGATGATGAGGATTAAAATGAGGGAAGGAGG	; SOFTWARE: PatentIn Release #1.0, Version #1.25
Qy         109 lProProAspThrLysLeuSerLysLeuAspThrLeuArgLeuAlaSerSerTyrIleAl 129           Db         420 CTCCAAAACATGTCTAAGATTGAAACTCTGCGCCTGGCTAAGAACTACATCTG 479           Qy         129 aHisLeuArgGlnIleLeuAlaSenAspLysTyrGluAsnGlyTyrIleHisPr 147           Db         480 GGCTCTTCTGAGATTTAAGGTCCGCCAAAAGCCCAGACCTGGTGTCCTTTGTACAAC 539           Qy         147 ovalAsnLeuThrTrpProPheMetValAlaGlyLy 159           Db         540 TCTCTGCAAAGGTTTGTCGCACCACCACCACCACCACCACCACCACCACCACCACCA	RESULT 5 US 009-499-273 US 009-499-274 US 009-499-499-499 US 009-499-49	

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135 CTCAGTTCTCAGGACGAGGAGCACGAGGACAAGAAGGAGGACGACGTCGAAGCATG 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 LeuSerAspValGluAspLeuGlnGluValGluMetLeuGluCysAspGlyLeuLysMet
        500 CCCCAGAACTTTCCTTCCTGAGCAGAGTCAGGACATCCAGTCGCACATGC 649
                                                                                                                                                   APPLICANT: Weintraub, Harold M.
APPLICANT: Lee, Jacqueline E.
APPLICANT: Tapscott, Stephen J.
APPLICANT: Hollenberg Stanley M.
APPLICANT: Hollenberg Stanley M.
TITLE OF INVENTION: Neurogenic Differentiation (NeuroD) Genes
                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Christensen O'Connor Johnson KindnessPLLC
STREET: 1420 Fifth Avenue, Suite 2800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

CLASSIFICATION DATE:

CLASSIFICATION NUMBER:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

APPLICATION NUMBER:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

APPLICATION NUMBER:

APPLICATION NUMBER:

APPLICATION NUMBER:

APPLICATION NUMBER:

REGISTRATION NUMBER:

REGISTRATION NUMBER:

REGISTRATION NUMBER:

TELEPOWNUMICATION NUMBER:

TELEPOWNUMICATION NUMBER:

TELEPOWNUMICATION NUMBER:

TELEPOWNUMICATION NUMBER:

TELEPOWNUMICATION SEQ 1D NO:

TELEPACOMMUMICATION SEQ 1D NO:

TELEPACE COMMUMICATION:

TELEPACOMMUMICATION SEQ 1D NO:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-701-674A-23 (1-179) x US-08-552-142A-14 (1-1560)
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ndels:
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                                                                                       , Sequence 14, Application US/08552142A
; Patent No. 5695995
                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 98101-2347
COMPUTER READABLE FORM:
MSDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.16e-08
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50.37%
30.37%
15.98%
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                                                                                                                                                                                                                                                                                                   ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRES
ADDRESSEE: Christe
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                            Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: line
MOLECULE TYPE: <
ORIGINAL SOURCE:
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STRANDEDNESS:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05741
FILING DATE:
CLASSIFICATION:
ATTORNEY/SAGNT INPORMATION:
NAME: Broderick Thomas F.
REGISTRATION NUMBER: 31,332
REFERENCE/DOCKET NUMBER: FHCR-1-8504
TELEPANINICATION INPORMATION:
TELEPANINICATION INPORMATION:
TELEPANINICATION OF SEQ 100
INFORMATION FOR SEQ 10 NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1275 base pairs
TYPE: nucleic acid
STRANDENNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.64e-09
154.00
46.46%
33.84%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
25..1083
                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
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Best Local Similarity:
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
Pred. No.:
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Sequence 14, Application US/09499227

Sequence 14, Application US/09499227

Patent No. 6444463

GENERAL INFORMATION:
APPLICANT: Tapscott, Stephen J.
APPLICANT: James M.
TITLE OF INVENTION: Expression of Neurogenic bHLH Genes in Primitive Neuroectoder NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Christensen O'Connor Johnson KindnessPLLC
STREET: 1420 Fifth Avenue, Suite 2800
                                                                                                                                                                                                                                                                                                                                                                                                                         195 AACGCAGAGGAGGACTCACTGAGGAACGGGGGAGGAGGAGGACGAGAAGATGAGGACCTG 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            255 GAAGAGGAGGAAGAAGAGAAGAGGATGACGATCAAAAGCCCAAGAGACGCGGCCCC 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AsnAlaArgGluArgAlaArgMetArgValLeuSerLysAlaPheSerArgLeuLysThr 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .05 ThrieuProTrpValProProAspThriysLeuSeriysLeuAspThrieuArgLeuAla 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26 AspSerAsnLysGluPheVal --- ThrSerAsnGluSerThrGluGluSerSerAsnCys 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45 GluAsnGlySerProGlnLysGlyArgGlyGlyLeuGlyLysArgArgLysAlaProThr 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       375 AACGCCCGGGAGCGGAACCGCATGCACGGACTGAACGCGGCGCTAGACAACCTGCGCAAG
                                                                                                                                                                                                                                                                                                                                                                                         LeuSerAspValGluAspLeuGlnGluValGluMetLeuGluCysAspGlyLeuLysMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 LysLysSerProLeuSerGlyValSerGlnGluGlyLysGlnValGlnArgAsnAlaAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     495 AAGAACTACATCTGGGCTCTGTGGGGGATCCTGCGCTCAGGCAAA 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 SerSerTyrlleAlaHisLeuArgGlnIleLeuAlaAsnAspLys 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 05-August-1998
PRIOR APPLICATION NUMBER: US 08/239,238
FILING DATE: 06-May-1994
                                                                                                                                                                                                                  Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                  US-09-701-674A-23 (1-179) x US-08-910-973-14 (1-1560)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 98101-2347
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                  146.50
50.37%
30.37%
15.98%
ORGANISM: Homo sapiens
                                                                                                          57..1126
                  ; IMMEDIATE SOURCE:
; CLONE: HC2A
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 57.111
US-08-910-973-14
                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                           Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Tapscott, Stephen J.
APPLICANT: Olson, James M.
TITLE OF INVENTION: Expression of Neurogenic bHLH Genes in Primitive Neuroectoder NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Christensen O'Connor Johnson KindnessPLLC
                                                                                                                                                                                                                     315 AAAAAGAAGAAGATGACTAAGGCTCGCCTGGAGCGTTTTAAATTGAGACGCATGAAGCT 374
                                                                                                                                                                                                                                                                                                                                                                                255 GAAGAGGAAGAAGAGGAAGAAGAGGATGACGATCAAAAAGCCCAAGAGACGCGGCCCC 314
                                                                                                                                                                                                                                                                 85 ASRAlaArgGluArgAlaArgMetArgValLeuSerLysAlaPheSerArgLeuLysThr 104
                                                                                                                                                                                                                                                                                            105 ThrLeuProTrpValProProAspThrLysLeuSerLysLeuAspThrLeuArgleuAla 124
                                                                                                                                                                           84
                                                                                   GluAsnGlySerProGlnLysGlyArgGlyGlyLeuGlyLysArgArgLysAlaProThr 64
26 AspSerAsnLysGluPheVal -- - ThrSerAsnGluSerThrGluGluSerSerAsnCys 44
                                                                                                                                                                           LysLysSerProLeuSerGlyValSerGlnGluGlyLysGlnValGlnArgAsnAlaAla
                                                                                                                                                                                                                                                                                                                                                                                                                                          125 SerSerTyrIleAlaHisLeuArgGlnIleLeuAlaAsnAspLys 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Christensen O'Connor Johnson KindnessPLLC
STREET: 1420 Fifth Avenue, Suite 2800
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM IYPE: Floppy disk
COMPUTER: IBM PC compatible
PC-DOS/MG-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 35,356
REPERRENCE/DOCKET NUMBER: FHCR-1-10958
TELECOMMINICATION INFORMATION:
TELEPHONE: 206-682-8100; 206-224-0735 (direct)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA;
APPLICATION NUMBER: US 08/239,238
FILING DATE: 06-MAY-1994
PRIOR APPLICATION DATA;
APPLICATION NUMBER: WO PCT/US95/05741
FILING DATE: 08-MAY-1995
PRIOR APPLICATION DATA;
APPLICATION NUMBER: PCT/US96/17532
FILING DATE: 30-October-1996
ATTORING PAPLICATION NUMBER: PCT/US96/17532
FILING DATE: 30-October-1996
ATTORING YAGENT INFORMATION:
REGISTRATION NUMBER: 35,356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 14, Application US/08910973
Patent No. 5795723
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 206-225-0779
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
E: cDNA
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ORIGINAL SOURCE:
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Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: gene
LOCATION: (0)...
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Pred. No.:
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US-08-552-142A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          375 AACGCCCGGGAGCCGCATCCACGGACTGAACGCGGCGCCTAGACAACCTGCGCAAG 434
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US95/05741
FILING DATE: 08-May-1995
PRIOR APPLICATION NUMBER: WO PCT/US96/17532
APPLICATION NUMBER: PCT/US96/17532
FILING DATE: 30-October-1996
PRIOR APPLICATION NUMBER: US 08/910,973
FILING DATE: 07-August-1997
ATTORNEY/AGENT INFORMATION:
NAMME: Sheliness, Diana K.
REGISTRATION NUMBER: 35,356
REFERENCE/DOCKET NUMBER: FHCR-1-12742
TELECOMMUNICATION INFORMATION:
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS: LENGRYH: 1560 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear MOLECULE TYPE: cDNA ORIGINAL SOURCE:
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146.50
50.378
30.378
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IMMEDIATE SOURCE:
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; LOCATION: 57..1126
US-09-499-227-14
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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85 AsnAlaArgGluArgAlaArgMetArgValLeuSerLysAlaPheSerArgLeuLysThr 104
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GENERAL INFORMATION:
APPLICANT: Cedars-Sinai Medical Center
APPLICANT: Michel F. Levesque, M.D.
APPLICANT: Michel F. Levesque, M.D.
TITLE OF INVENTION: CONVERSION OF NON-NEURONAL CELLS INTO
TITLE OF INVENTION: NEURONS; TRANSDIFFERENTIATION OF EPIDERMAL CELLS
FILE REPERENCE: P07 41494
CURRENT APPLICATION NUMBER: US/09/234,332A
CURRENT FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
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| Sequence 1. Application US/0855142A
| Patent No. 5655955
| GENERAL INFORMATION:
| APPLICANT: Weintraub, Harold M. APPLICANT: Tapscort, Stephen J. APPLICANT: Hollenberg, Stanley M. APPLICANT: Hollenberg, Stanley M. TITLE OF INVENTION: Neurogenic Differentiation (NeuroD) Genes TITLE OF INVENTION: and Proteins
| NUMBER OF SEQUENCES: 20 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             125 SerSerTyrileAlaHisLeuArgGlnileLeuAlaAsnAspLys 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (0)...(0)
OTHER INFORMATION: Neuro D1 gene: Genbank accession D82347
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Matches:
Conservative:
Mismatches:
Indels:
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146.50
50.37%
30.37%
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APPLICANT: Tapscott, Stephen J.
APPLICANT: Tapscott, Stephen J.
APPLICANT: Tapscott, Stephen J.
APPLICANT: Olson, James M.
TITLE OF INVENTION: Expression of Neurogenic bHLH Genes in Primitive Neuroectoder INTRES OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
10 GluAspLeuGlnGluValGluMetLeuGluCysAspGlyLeuLysMetAspSerAsnLys 29
                                                                                                                                                                                                                                                                                                                                        B: Christensen O'Connor Johnson KindnessPLLC 1420 Fifth Avenue, Suite 2800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Sheiness, Diana K.
REGISTRATION NUMBER: 35,356
REPERENCE NUMBER: FFCR-1-10958
TELECOMUNICATION INCREATION:
TELECOMUNICATION INCREATION:
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Mismatches:
Indels:
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                                                                130 HistenArgGlnileLeuAlaAsnAspLys 139
                                                                                        682 GCTCTGTCAGAGATCCTGCGCTCAGGCAAA 711
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Matches:
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PRICR APPLICATION DATA:
PAPPLICATION NUMBER: US 08/239,238
FILING DATE: 06-MAY-1994
PRICR APPLICATION NUMBER: WO PCT/US95/05741
FILING DATE: 08-MAY-1995
PRICR APPLICATION DATA: POT MAY 1995
PRICR APPLICATION DATA: PCT/US96/17532
FILING DATE: 30-October-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                           Sequence 1, Application US/08910973
Patent No. 5795723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 206-682-8100; 3 TELEFAX: 206-25-0779 INFORMATION FOR SEQ ID NO: 1: SEGUENCE CHARACTERISTICS: LENGTH: 2089 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 2347
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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49.23%
34.62%
15.92%
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229..1302
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STREET: 1420 Fi
CITY: Seattle
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: line MOLECULE TYPE: c ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                             CITY: Sea
STATE: WA
COUNTRY:
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                                                                                                                                                                 -08-910-973-1
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      ADDRESSEE: Christensen O'Connor Johnson KindnessPLLC
STREET: 1420 Fifth Avenue, Suite 2800
CITY: Seattle
                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/552,142A
PILING DATE: O2-NOV-1995
CLASSIFICATION: 514
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-701-674A-23 (1-179) x US-08-552-142A-1 (1-2089)
                                                                                                                                                                                                                                                         FILING DATE: 02-NOV 1995
CLASSIFICATION: 514
PRIOR APPLICATION 1514
APPLICATION NUMBER: US 08/239,238
FILING DATE: 06-MAY-1994
FRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US95/05741
FILING DATE: 08-MAY-1995
ATTONNEY/AGENT INPORMATION:
NAME: Broderick, Thomas F.
REGISTRATION NUMBER: 31,332
RESPERNEYS DOCKET NUMBER: PHCR-1-8933
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 206-225-0709
INFORMATION POR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2089 base pairs
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49.23%
34.62%
15.92%
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MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
EDNESS: double
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229..1302
                                                                                                       ZIP: 98101-2347
COMPUTER READABLE FORM:
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Best Local Similarity:
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                                                                                      USA
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Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
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                                                                    STATE: W
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90 AlaArgMetArgValLeuSerLysAlaPheSerArgLeuLysThrThrLeuProTrpVal 109
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GENERAL INFORMATION:
APPLICANT: Weintraub, Harold
APPLICANT: Lee, Jacqueline E.
APPLICANT: Tapscott, Stephen J.
APPLICANT: Hollenberg, Stanley M.
TITLE OF INVENTION: Neurogenic Differentiation (NeuroD) Gene
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45
19
58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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Conservative:
Mismatches:
Indels:
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49.23%
34.62%
15.92%
                                                            MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: Mus musculus
nucleic acid
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229..1302
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CORRESPONDENCE ADDRESS:
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                                              linear
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ZIP: 98101-2347
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Best Local Similarity:
                         STRANDEDNESS:
TOPOLOGY: lir
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                                                                                                                                                                           ; LOCATION:
US-09-499-227-1
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APPLICANT: Olson, James M.
TITLE OF INVENTION: Expression of Neurogenic bHLH Genes in Primitive Neuroectoder
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                         110 ProProAspThriysieuSeriysLeuAspThrieuArgieuAlaSerSerTyrileAla 129
                    GAGGACGAGCTTGAAGCCATGAATGCAGAGGAGGACTCTCTGAGA----AACGGGGGGAGAG 402
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502 ACCAAGGGGCGCCTAGAAACGTTTTAAATTAAGGCGCATGAAGGCCAACGCCCGCGAGCGG 561
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                                                                GluPheValThrSerAsnGluSerThrGluGluSerSerAsnCysGluAsnGlySerPro 49
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MEDIUM TYPE: 1810py disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SUSTWARE: Patentin Release #1.0, Version #1.25
SUSTWARE: Patentin Release #1.0, Version #1.25
SUSTRANT APPLICATION DATA:
APPLICATION NUMBER: US 08/239,238
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/239,238
FILING DATE: 06-May-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US96/17532
FILING DATE: 30-October-1996
PRIOR APPLICATION NUMBER: US 08/910,973
FILING DATE: 310-October-1997
ATPONEY/AGENTIND NUMBER: US 08/910,973
FILING DATE: US 08/910,973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAMES: Sheiness, Diana K.
REGISTRATION NUMBER: 35,356
REFERENCE/DOCKET NUMBER: FHCR-1-12742
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-682-8100, 206-224-0735 (direct)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 HistenArgGlnileLeuAlaAsnAspLys 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 644463
GENERAL INFORMATION:
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86 aArgGluArgAlaArgMetArgValLeuSerLysAlaPheSerArgLeuLysThrLe
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SEB: Christensen O'Connor Johnson KindnessPLLC
; 1420 Fifth Avenue, Suite 2800
Seattle
                                                                                                                                                                                CONDITY: 0.247

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/552,142A
FLING DATE: 02-NOV-1995
CLIASSIPICATION DATA:
APPLICATION NUMBER: US 08/239,238
FILING DATE: 06-May-1994
FRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US95/05741
FILING DATE: 08-May-1994
FRIUNG DATE: 08-May-1995
FILING DATE: 08-May-1995
FILING DATE: 18-May-1995

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Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 206-225-0709
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
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32.418
15.878
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STRANDEDNESS: single
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MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
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Best Local Similarity:
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US-08-552-142A-16
            ADDRESSEE:
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Pred. No.:
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DB:
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502 ACCAAGGGGGCGCTAGAAGGTTTTAAATTAAGGCGCATGAAGGCCAACGCCCGCGAGGGG
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Weintraub, Harold M.
APPLICANT: Tapscott, Stephen J.
APPLICANT: Hollenberg, Stanley M.
TITLE OF INVENTION: Neurogenic Differentiation (NeuroD) Genes TITLE OF INVENTION: and Proteins
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative:
Mismatches:
Indels:
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Matches:
                                                                                                                        ATTORNEY AGENT INFORMATION:
NAME: Broderick, Thomas F.
REGISTRATION NUMBER: 31,332
REFERENCE/DOCKET NUMBER: FHCR-1-8504
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-22-9100
TELEPAX: 206-22-0709
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
            APPLICATION NUMBER: PCT/US95/05741 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
US-08-52-142A-16
; Sequence 16, Application US/08552142A
; Patent No. 5695995
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146.00
49.23%
34.62%
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: 229..1302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
                                                                                                CLASSIFICATION:
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Pred. No.:
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PCT-US95-05741-1
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ò	143GlyTyrIleHisProVal-AsnLeuThrTrpProPheMetV 156
qa	797 CGTGCAGACTCTGTGCAAGGGGCTGTCACCCACCACCACGAATCTGGTGGCCGGCTGCCT 856
δλ	3lyLysProGluSerAspLeuLysGlu
qq	857 GCAGTTAAACTCTCGTAACTTCCTCACGGAGCAGCGC 895
λö	176 hrThrAlaSer 179
qa	896 GGACGGCGC 906
Search Job ti	Search completed: December 17, 2004, 00:05:29 Job time : 94 secs

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Murine mu

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Add5529 Human pol
Ab165519 Lung canc
Ab165919 Lung canc
Ab165919 Lung canc
Ab165919 Lung canc
Ab108723 Drosophil
Ab108723 Drosophil
Ab218599 Group III
Ad23083 Human nov
Ad25304 Human sof
Acc62291 Human sec
Acc6231 Human sec
Acc6231 Human sec
Ad32623 Human ost
Ad32651 Human ost
Ad41581 Human cDN
Ad41581 Human GDN
Ad49596 Rat dHAND
Abk1581 Human GDN
Ach89595 Human pas
Ad965591 Human pas
Ad965591 Human bas
Ad965591 Human bas
Ad965591 Human sof
Ad416814 Human man
Ad416814 Human man
Ad416814 Human man
Ad428651803 Human Mada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein regulating gene expression; PRGE-23; human; cancer; inflammation; anticancer; antitumour; antiinflammatory; Myc; HLH protein; gene therapy; diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein regulating gene expression PRGE-23 cDNA clone 3340296.
AAZS0464
AAZS0465
AAZS0465
ACH21857
ACH218526
ABL65535
ABL65935
ABL65935
ABL65935
ABL65935
ABC62935
ABC6223
ABC18723
ABC18723
ABC18723
ABC18623
ABC3223
AAQ88217
ACC62491
ACC62491
AACC62438
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ADP65591
ADP65052
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ABT06509
ADM83716
ADQ17684
ABL16071
ABL6071
ADP65592
AAS94864
AAL62234
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268. .807
/*tag= a
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98US-0094575P.
98US-0104624P.
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                      1396
1664.
1800
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                               12-JUN-1998;
29-JUL-1998;
14-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9964596-A2
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 Command line parameters:

-MODEL=frame+ p2n.model -DEV-x1h
-Q=/CG12 1/UBFPTO spool h/USO9701674/runat 15122004 100440 27494/app query.fasta_1.327
-Q=/CG12 1/UBFPTO spool h/USO9701674/runat 15122004 100440 27494/app query.fasta_1.327
-DB=N Geneseq_23Sep04 -QFNT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCI=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LCCAL. -OUTFMT=pto -NOFM=ext -HarbSIZE=500 -MINIMENSE - MAXLEN=200000000
-USER=USO9701674 @CGN 1 1 470 @runat 15122004 100440 27494 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQÜERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THRRADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAFOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Abq55427 Human ova
Ade25693 Human cDN
Aaa7428 Human nuc
Adj56314 Human cDN
Aas94828 Human DNA
                                                                      December 16, 2004, 20:16:52 ; Search time 455 Seconds (without alignments) 2065:157 Million cell updates/sec
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917
1 MSTGSLSDVEDLQEVEMLEC......PESDLKEVVTASRLCGTTAS 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
                                                                                                                                                                                                                                                      8269772
          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                    OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                  hits satisfying chosen parameters:
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Listing first 45 summaries
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ABQ55427
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ADJ56314
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 200000000
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Match Length DB
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Database :

Result No.

Total number

Searched:

Sequence:

Title:

Run on:

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New human polypeptides that regulate gene expression, for treatment, prevention and diagnosis of, e.g. cancer.
           Bandman O,
Patterson C,
           Hillman JL,
Baughn MR,
(INCY-) INCYTE PHARM INC.
           Yue H, Tang YT,
KJ, Gorgone GA,
                              WPI; 2000-116543/10.
                                     P-PSDB; AAY58630
                   Guegler
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Corley NC; Lu DAM;

9; Page 139; 150pp; English Claim

The present sequence is that of Incyte clone 3340296 encoding new human procein regulating gene expression PRGB-23 (see AAY58630). The CDNA was initially isolated from spleen tissue cONA library SPLNNOTIO, and the full-length sequence assembled from overlapping clones from a number of libraries. PRGB-23 is expressed in reproductive, developmental and usrologic tissues associated with cancer, inflammation and foctal diseases, disorders or conditions. It is characterised as an Myc-type Hipprocleotides (see AAX57819-69), expression vectors, host cells, polymucleotides (see AAX57839-69), expression vectors, host cells, antibodies, agonists and antagonists. It also provides methods for diagnosing, treating or preventing disorders associated with expression of PRGB. Polymucleotides are also used as sources of probes and primers for diagnosis and monitoring of disease, also for detecting related sequences and in gene mapping

Sequence 1272 BP; 311 A; 358 C; 318 G; 285 T; 0 U; 0 Other;

1272 179 7e: 0 0 0		erThrdlySerLeuGerAspValGluAspLeuGlnGluValGluMetLeuGluCys 20 	AspGlyLeuLysMetAspSerAsnLysGluPheValThrSerAsnGluSerThrGluGlu 40 	SerSerAsnCysGluAsnGlySerProGlnLysGlyArgGlyGlyLeuGlyLysArgArg 60 	LysalabroThrLysLysSerbroLeuserGlyValSerGlnGluGlyLysGlnValGln 80 	ArgAsnAlaAsnAlaArgGluArgAlaArgMetArgValLeuSerLysAlaPheSer 100 	ArgleulysThrThrLeuProTrpValProProAspThrLysLeuSerLysLeuAspThr 120 	Leuargieualasersertyrilealahisieuargginileieualaasnaspiystyr 140 	GluasnGlyTyrIleHisProValasnLeuThrTrPProPheMetValalaGlyLysPro 160 
Length: Matches: Conservative Mismatches: Indels: Gaps:	861 (1-1272)	eraspValGluaspLeuGl 	erAsnLysGluPheVal 	1yserProglnLysgl) 	erProLeuSerGlyval: 	aArgGluArgAlaArgMetA                     GCGAGAGCGGGCCCGCATGC	rotrpvalProProAsp 	yrileAlaHisLeuArg 	roValasnieuThrTrp 
(cores: 4.19e-92 917.00 917.00 11]arity: 100.00\$ 11.11]arity: 100.00\$ 11.11]	-23 (1-179) x AAZ57861	MetSerThrGlySerLeuS 	AspolyLeuLysMetAspSerAsnLysGluPheVal 	SerSerAsnCysGluAsnGly 	LysalaproThrLysLysSerProLeuSerG  	ArgAsnAlaAlaAsnAlaA: 	argleulysThrThrLeuP                  GACTCAAGACCACCCTGC	LeuArgleuAlaSerSerT 	GluasnGlyTyr11eHisProvala G
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161 GluSerAspLeuLysGluValValThrAlaSerArgLeuCysGlyThrThrAlaSer 179

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treating, prognosing or preventing and purpoprises.

treating, prognosing or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertinity, disorders of pregnancy, ancoulation, polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine disorders, infertinons (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome). Inflammatory conditions (e.g., mastitis, opphoritis and vaginitis), immune disorders (e.g., congenital and acquired yrthematosus), blood-related disorders (e.g., congenital and acquired yrthematosus), commondeficiencies, autoimmune oophoritis, systemic lupus erythematosus), clond-related disorders. Gend uninary system disorders. Ovarian antigen polypeptides and collumication antigen expression or activity. The polynucleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polynucleotides may be used a food additives or to prepare antibodies clonding to dispage a food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP41228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also encompasses polypeptides 90% identical and polynuclectides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen polynuclectides, antibodies against human ovarian antigen of ovarian antigen polynuclectides and polypeptides in diagnosing,
                                                                                                                                                                                                                                                                                                                                                           syndrome;
748 GAGAGTGACCTGAAAGAAGTGGTGACCGCGAGCCGCTTATGTGGAACCACCGCGTCC 804
                                                                                                                                                                                                                                                                                                    Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anountation; polyoystic ovary syndron PCOS; ovarian cyst; dysmenorthoea; endocrine disorder; infection; inflammatory condition; namune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; infiniary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive; gene; ss.
                                                                                                                                                                                                                                                             Human ovarian antigen HNOJ185 cDNA, SEQ ID NO:1307.
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                                                                                                                         ABQ55427 standard; cDNA; 632
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P-PSDB; ABP42350.
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Shiffman 2003-875398/81

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Mikita

19-SEP-2001; 2001US-0323784P.

(INCY-) INCYTE GENOMICS INC.

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invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                       AspGlyLeuLysMetAspSerAsnLysGluPheValThrSerAsnGluSerThrGluGlu
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 represents cDNA encoding a human ovarian antigen of the
                                                               U; 17 Other;
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Matches:
Conservative:
Mismatches:
Indels:
                                                             Sequence 632 BP; 145 A; 176 C; 201 G; 93 T; 0
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91.62%
91.06%
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                                                                                       Scores:
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The invention relates to a combination comprising several polymucleotides having any one of 127 sequences (S1) such as the sequence of human call and the control of the sequence of human call and the control of the sequence of human call control of the sequences and extended or full length gene from a library of mucleic acid sequences, an expression vector containing the nucleic acids, a host cell containing the vector, a purified polypeptide appearing as ADE25750 and ADE25751, producing a profit of polypeptide appearing as ADE25750 and composition comprising a purified antibody that specifically binds to the proteins. The foam cell-expressed nucleic acids are useful for a high throughput detection of differential expression of one or more polymucleotides in a sample. The sample is from a subject with a throughput screening of a library of molecules or compounds to identify a ligand which binds a polymucleotide. The library is chosen from DNA molecules, peptides, proteins and RNA molecules. The protein is compounds to identify at least one ligand which specifically binds a protein, for purifying a ligand from a sample for making a antibody. The compounds to identify at least one ligand which specifically binds a protein, for purifying a ligand from a sample for making a antibody. The compounds to identify at least one ligand which specifically binds a protein cardiovascular disorder. The foam cell-expressed nucleic acids are useful for a macroarray which can be used for detecting related cardiovascular disorder. The foam cell-expressed nucleic acids are useful search or a microarray which can be used for detecting related the proper of the process 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          atherosclerosis. The present sequence_represents a cDNA whose expression is upregulated in LPS treated foam cells.
                                                                                                                                                                                                                                                       Combination containing several polynucleotide that are differentially expressed in foam cells and complements of the polynucleotides, useful for diagnosing cardiovascular disease or atherosclerosis.
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Indels:
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P-PSDB; ADE25769.
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560 GAGCGCAGCTACGCCTCGCCCAGTGACAACTCGTCGGCAGAGGAGGAGGACCCCCGACGGC 619

AspSerAsnLysGluPheValThrSerAsnGluSerThrGluGlu----

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::: 500 CGGGGGTGCAGCGGGAGTACCCGGTCCCCGCCTCCAAGAGGCCGCCCTCCGCGGGGGTA

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------ATGGAGCTT 499

MetSerThrGlySerLeuSerAspValGluAspLeuGlnGluValGluMetLeuGluCys

Gaps: (1-2177)

US-09-701-674A-23 (1-179) x ADE25693

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Similarity:

Best Local

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21 AspGlyLeuLys----

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                                                        98
    67
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ProGln---LysGlyArgGlyGlyLeuGlyLysArgArgLysAlaProThrLysLysSer
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P-PSDB; AAB21043.
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Sequences AAA72382-A72436 represent cDNAs encoding novel human nucleic acid-binding proteins (NAABPs, AAB20997-B21051). These cDNAs were produced by extension from an appropriate EST (expressed sequence tag) using primers designed using the EST. The invention also relates to expression constructs, host cells and transgenic organisms comprising a

Claim 4; Page 176; 180pp; English.

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the human NuABP nucleic acid, recombinant production of the human NuABPS, and also to methods of screening antibodies against the human NuABPS, and also to methods of screening condulators of human NuABPs, and their agonists and antagonists are used to treat diseases associated with coverexpression or underexpression of functional NuABPs. Human NuABP coverexpression or underexpression of functional NuABPs. Human NuABP coverexpression or underexpression of functional NuABPs. Human NuABP coverence and prevent reproductive, immunological, neurological and cell proliferative disorders. Reproductive disorders that may be treated using compositions of the invention include infertility, condematriosis, disruptions of the menstrual cycle and disruptions of disease and systemic luupus erythematosus.

Neurological disorders that may be treated include epilepsy, neurodegenerative conditions such as Alzheimer's disease and Parkinson's disease, prion diseases such as Cheutzfeldt-Jakob disease, and mental cycle atherosclerosis, cirrhosis and psociasis
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Human cDNA differentially expressed in MYCN activated cells SegID 120.
                                                                                                human, differential expression, transactivator, proto-oncogene;
neuroblastoma; small cell lung cancer; cytostatic; gene therapy; ss;
MYCN activated cell.
1040 GTTTCCGCAGCCAACAGCTATGTGGAACCACCGCT 1075
                                                                                                                                                                                                                                            Shohet JM;
                                                                                                                                                                                                                                            Plon SE,
                                     ADJ56314 standard; cDNA; 2196
                                                                                                                                                                          25-FEB-2002; 2002US-00084817.
                                                                                                                                                                                        23-FEB-2001; 2001US-0270784P.
                                                                  06-MAY-2004 (first entry)
                                                                                                                                                                                                                                            Stuart SG, Nuchtern JG,
                                                                                                                                                                                                      (STUA/) STUART S G.
(NUCH/) NUCHTERN J G.
(PLON/) PLON S E.
(SHOH/) SHOHET J M.
                                                                                                                                                                                                                                                            WPI; 2003-635698/60
                                                                                                                                             US2003119009-A1.
                                                                                                                               Homo sapiens.
                                                                                                                                                           26-JUN-2003
                                                     ADJ56314;
                                ADJ5631
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New genes regulated by MYCN activation, useful in gene therapy, particularly for treating a subject with e.g. neuroblastoma or other cancers, or for diagnosing, staging or monitoring the treatment of the

Claim 1; SEQ ID NO 120; 27pp; English

cancer

This invention relates to novel isolated cDNAs that are differentially expressed in MYCN activated cells. Specifically, it refers to polymocleotide sequences that exhibit differential expression patterns in cells activated by the transactivator MYCN, where MYCN is a protononcogene that is amplified in neuroblastoma cells and is common in small cells and to common in small cells ung cancers. The present invention describes these cDNA molecules or useful for in hybridisation assays to detect expression of nucleic acids (or complementary nucleic acids) in a present in a given sample, as useful for in hybridisation assays to detect expression of nucleic specifically bind the cDNA as a ligand and modulate function or activity. Accordingly, these compositions exhibit cytostatic activity and can also be used for gene therapy purposes. This polymucleotide sequence is a cDNA that is differentially expressed in MYCN activated cells, given in an exemplification of the invention. NOTE: This sequence does not appear in the printed specification but has been obtained in electronic format from the United Speciment Office. ftp.seqdata.uspto.gov/sequence.html?DocID=20030119009

Sequence 2196 BP; 438 A; 691 C; 653 G; 414 T; 0 U; 0 Other;

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2196
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       Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                 Gaps:
         7.08e-47
              514.00
63.21%
53.30%
56.05%
                     Percent Similarity:
Best Local Similarity:
Query Match:
Alignment Scores:
Pred. No.:
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US-09-701-674A-23 (1-179) x ADJ56314 (1-2196)

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LeuGluCys :::    ATGGAGCTT	Met	CCGACG	snGlySe	3GAAGC(	ystysse       AGAAGCO	laAsnA.	CCAACG	hrThrL	laSerS	CTTCCA	LYTYTIBHIS	euLysg.	 ccaaag						tion.	troke; y; ds.							Mikita	
GluMetLeuGlu       : : :  ATGGAC	: 5	BAGGACC	yşGluA	GCAAGA	ProThrL	AsnAlaA	AACGCGG	LeuLysT	ArgleuA	GGCTGG	AsnGlyT	SerAspl	CTGACA						erentia	ebral st therapy							GJ,	
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        Composition useful for diagnosis of conditions, disorders or diseases associated with atherosclerosis, comprises several polynucleotides that are differentially expressed in foam cell development.
                                                                                                 The present invention relates to the isolation of human polynucleotide sequences that are differentially expressed during feam cell differentiation. The polynucleotide sequences of the invention or a composition comprising these polynucleotides are useful as a high throughput method for detecting altered expression of one or more polynucleotides in a sample. The polynucleotides can be used in the diagnosis of disorders associated with foam cell development such as atherosclerosis, cerebral stroke, and cardiovascular disorders such as coronary artery disease. The polynucleotide sequences can also be used PCR primers and probes. The polynucleotide sequences can also be used useful in gene therapy. AAS$4746-AAS$5021 represent the human polynucleotide sequences of the invention are also polynucleotide sequences of the invention which are differentially expressed during foam cell differentiation
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The present cDNA sequence encodes murine musculin bHLH (basic helix-loophelix) protein, which is a transcription factor associated with genes from the lused in myogenesis. Musculin gene can be used in genetic screening for myogenic disease conditions, for detecting abberations in muscle development and in gene therapy. Anti-musculin antibodies can be used as therapeutic or dispostic agents. Musculin has cytostatic activity and can be used to treat myogenic disease conditions like myopathies, muscular dystrophies, neuromuscular and skeletomuscular disorders and
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/product= "Murine musculin bHLH protein"
/note= "Lacks Alanine-Threonine myogenic recognition
motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New regulatory protein useful for gene therapy of myogenic cancer detecting aberrations in muscle development in myogenic disease, comprises protein associated with genes involved in myogenesis.
rAspleulysGluValValThrAlaSerArgLeuCysGlyThrThrAla
               1031 IGACACCAAAGAAGTTTCCGCAGCCAACAGAACTATGTGGAACCACCGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       410 AAGCICICCAAGCIGGACACGCICCGGCIGGCIICCAGIIACAICGCICACCIGCGGCAG 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PheMetValAlaGlyLysProGluSerAspLeuLysGluValValThrAlaSerArgLeu 173
  and for
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                                                                                                                         The present cDNA sequence encodes human musculin bHLH (basic helix-loop helix) protein, which is a transcription factor associated with genes involved in myogenesis. Musculin gene can be used in genetic screening for myogenic disease conditions, for detecting abberations in muscle development and in gene therapy. Anti-musculin antibodies can be used a therapeutic or diagnostic agente. Musculin has expostatic activity and can be used to treat myogenic disease conditions like myopathies, muscular dystrophies, neuromuscular and skeletomuscular disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LysLeuSerLysLeuAspThrLeuArgLeuAlaSerSerTyrIleAlaHisLeuArgGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ::: ||| ||| ||| ||| ||| ||| AGIGACACGACGCGAGGAGGAGGAGCGCTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  290 GCAGAGTGCAAGCAGTCGCAGCGGAACGCGGCCAACGCCCGTGAGCGTGCCGGATGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ValleuSerLysAlaPheSerArgLeuLysThrThrLeuProTrpValProProAspThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IleLeuAlaAsnAspLysTyrGluAsnGlyTyrIleHisProValAsnLeuThrTrpPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        170 GGCACAGCCGGCAGCGCGGAAGGCTGCAAGAGGAAGCGGCCCCCCGCGGGGGCTGGGGGCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlyLeuGlyLysArgLysAlaProThrLysLysSer---ProLeuSerGlyValSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlnGluGlyLysGlnValGlnArgAsnAlaAlaAsnAlaArgGluArgAlaArgMetArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTGCTGAGCAAAGCCTTCTCCAAGGCCTAAGACCAGCCTGCCCTGGGTGCCCCCCGACACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -------SerSerAsnCysGluAsnGlySerProGln---LysGlyArgGly
  cancer
New regulatory protein useful for gene therapy of myogenic cances detecting aberrations in muscle development in myogenic disease, comprises protein associated with genes involved in myogenesis.
                                                                                                                                                                                                                                                                                                                                                518 G; 312 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                              1716
102
14
30
19
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                       English,
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                                                                                       Example 3; Page 38-40; 54pp;
                                                                                                                                                                                                                                                                                                                                                   Sequence 1716 BP; 336 A; 550
                                                                                                                                                                                                                                                                                                                                                                                                          9.67e-45
493.50
70.30%
61.82%
53.82%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity:
                                                                                                                                                                                                                                                                                                       myogenic cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
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DB:
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80
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The invention relates to an isolated polymucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH5081, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polympetide comprising a sequence corresponding to a reading frame of the novel polymucleotide. The nucleic acid sequences care useful in diagnostics as expressed sequence tags (BST) for identifying expressed gene or for physical mapping of the human genome, in fernatics, in assessing bloidiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, for formomesm and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. The purified polypeptide is useful for generating antisense DNA or RNA. The purified polypeptide is useful for generating antisense specific for it. The present sequence is one of the 38043 isolated CDNA/BST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from userio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating
                                                                                                                                                                              SBH; expressed sequence tag; EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stache-Crain B, Dickson MC, Jones LW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 482 BP; 99 A; 156 C; 143 G; 83 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  obtained in electronic format directly from USPTO at segdata.uspto.gov/sequence.html?DocID=20030073623
                                                                                                                                                                          Human; ss; sequencing by hybridisation; SBH; ey
genome mapping; biodiversity; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 9069; 44pp; English.
                    ACH21857 standard; cDNA; 482 BP
                                                                                                                                                                                                                                                                                                                                                      30-JUL-2001; 2001US-00918995
                                                                                                                                                                                                                                                                                                                                                                                            30-JUL-2001; 2001US-00918995
                                                                                                                                       Human adult ovary cDNA #237.
                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    LABAT I.
STACHE-CRAIN B
DICKSON M C.
JONES L W.
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antisense DNA or RNA
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                                                                                                                                                                                                                                      Homo sapiens.
                                                                                               13-OCT-2003
                                                                                                                                                                                                                                                                                                               17-APR-2003
                                                        ACH21857;
                                                                                                                                                                                                                                                                                                                                                                                                                                 (DRMA/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (STAC/)
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ACH21857
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482
95
1
0
0
0
                Matches:
Conservative:
Mismatches:
         Length:
                                        Indels:
                                               Gaps:
       8.84e-45
487.00
98.96%
53.11%
                      Percent Similarity:
Best Local Similarity:
Alignment Scores:
                                        Query Match:
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84 AlaAsnAlaArgGluArgAlaArgMetArgValLeuSerLysAlaPheSerArgLeuLys 103 GCCNTAGGGGGAGAGCGGGCCCGCATGCGAGTGCTGAGCAAGGCCTTCTCCCAGACTCAAG 92

US-09-701-674A-23 (1-179) x ACH21857 (1-482)

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93 ACCACCCTGCCCTGGGTGCCCCCCGACACCTCTCCAAGCTGGACACGCTCAGGCTG 152
                                              143
                                                                     212
                                                                                             TyrileHisProValAsnLeuThrTrpProPheMetValAlaGlyLysProGluSerAsp 163
                                                                                                                    213 TACATTCACCCGGTCAACCTGACGTGGCCCTTTATGGTGGCCGGGAAACCCGAGAGTGAC 272
                                                                                                                                                                                                                                                                                                                Chicken; probe; ss; array element; Parkinson's disease; signalling pathway population; cancer; adenocarcinoma; leukaemia; immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
 ThrThrLeuProTrpValProProAspThrLysLeuSerLysLeuAspThrLeuArgLeu
                                               AlaSerSerTyrIleAlaHisLeuArgGlnIleLeuAlaAsnAspLysTyrGluAsnGly
                                                                GCGTCCAGCTACATCGCCCACTTGAGGCAGATCCTGGCTAACGACAAATACGAGAAACGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Combination of polynucleotide probes, useful as array elements in microarray for monitoring the expression of a number of target polynucleotides.
                                                                                                                                                                                                                                                                                          Chicken signalling pathway polynucleotide probe SEQ ID NO 1028.
                                                                                                                                         LeuLysGluValValThrAlaSerArgLeuCysGlyThrThrAlaSer 179
                                                                                                                                                                   creaaaaaaadregreaceeeageeerrareregaaceaceeege
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 1028; 65pp; English.
                                                                                                                                                                                                                  ACA56430 standard; cDNA; 240 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-00016434.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-00016434.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Au-Young J, Seilhamer JJ;
                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                 Sallus gallus.
                                                                                                                                                                                                                                                                  06-JUN-2003
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                                                                                                                                                                                                                                           ACA56430;
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The invention relates to a combination which, comprises a number of polymucleotide probes comprising a sequence selected from one of the 1490 sequences mentioned in the specification. The combination is useful as an seray element in a microarray for monitoring the expression of a number of target polymucleotides. The microarray is particularly useful in the diagnostic and immunopathology and neuropathology. The microarray is useful in diagnostics and treatment regimens, drug discovery and development, toxicological and carcinogenicity studies, of oremsics and pharmacogenomics. The microarray is also useful for monitoring progression of diseases and for developing sophisticated profiles for the effects of currently available therapeutic drugs. The combination is also useful for purifying a subpopulation of mRNAs, cDNAs array can detect changes in expression in a large number of genes coding for different signaling pathway populations which can be used to diagnose or and penomic fragments and in research and diagnostic applications. The array can detect changes in expression in a large number of genes coding for different signaling pathway populations which can be used to diagnose or and parkinson's disease and penalties e.g. AIDS and aathma, neuropathies e.g. Alzhainer's disease and Parkinson's disease. The present sequence represents a polynucleotide form part of the printed Segmence and a to this patent did not form part of the printed sequence data for this patent did not form at directly from USPTO at

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comprising at least a portion of a gene encoding a transducing comprising at least a portion of a gene encoding a transducing polypeptide and third polymucleotide probes comprising at least a portion of a gene encoding an effector-like polypeptide. The probes of the composition are useful as array elements in a microarray for monitoring the expression of target polymucleotides. The microarray for monitoring classical and cardent, an immunopathology or a neuropathology. It can also be used for drug discovery and development, contrological and carcinogenicity studies, forensics or pharmacogenomics. Microarrays can also be used for monitoring the progression of diseases that may be associated with the anitoring the progression of diseases that may be associated with the altered expression of signalling pathway polypeptides. The composition can also be used to purify a subpopulation of manns, constitution of a sample. The expression profile is also useful for the diagnosis and treatment of cancer, e.g. cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast or cervix, an immunopathology, e.g. dementia, amnesta, epilepsy, Alzheimer's disease or depression. This sequence represents a chiman polymucleotide probe of the invention. Note: The sequence data for this patent did not form part of the printed specification but was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           erArgLeuLysThrThrLeuProTrpValProProAspThrLysLeuSerLysLeuAspT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCAGACTCAAGACCACCTGCCTGGGTGCCCCCGGACACCAAGCTCTCCAAGCTGGACA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hrLeuArgLeuAlaSerSerTyrlleAlaHisLeuArgGlnIleLeuAlaAsnAspLys 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, cancer, colon, breast, ovary, oesophagus, kidney, thyroid, stomach, lung, prostate, pancreas, carcinoma, antitumour, cancerous, cytostatic, gene therapy, antineoplastic, Wilm's tumour, adenocarcinoma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nArgAsnAlaAlaAsnAlaArgGluArg-AlaArgMetArgValLeuSerLysAlaPheS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LysAlaProThrLysLysSerProLeuSerGlyValSerGln-GluGlyLysGlnValGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lung cancer related gene sequence SEQ ID NO:3856.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-701-674A-23 (1-179) x ADI56226 (1-240)
                                                                                                                                                                                                                                                                                                                                                                                  72
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                                                                                                                                                                                                                                                                                                                                                                                    55 A; 83 C;
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353.00
93.83%
93.83%
12.12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                    Sequence 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; probe; ss; receptor-like polypeptide; transducing polypeptide; defector-like polypeptide; cancer; immunopathology; neuropathology; drug development; toxicology; carcinogenicity; signalling pathway polypeptide; adrenal gland; bladder; bone; signalling pathway polypeptide; adrenal gland; bladder; bone; diabetes; bone marrow; train; breast; cervix; tumnopathology; AIDS; diabetes; pancreatitis; osteoporosis; ulcerative colitis; neuropathology; dementia; amnesia; epilepsy; Alzheimer's disease; depression.
                                                                                                                                                                                                                                                                                                 nArgAsnAlaAlaAsnAlaArgGluArg-AlaArgMetArgValLeuSerLysAlaPheS 100
                                                                                                                                                                                                                                                                                                                                                                 erArgLeuLysThrThrLeuProTrpValProProAspThrLysLeuSerLysLeuAspT 120
                                                                                                                                                                                                                                                                                                                                                                                                  121 CCAGACTCAAGACCACCCTGCCCTGGGTGCCCCCCGACACCAAGCTCTCCAAGCTGGACA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New composition comprising polynucleotide probes, useful as array elements in a microarray for monitoring the expression of target polynucleotides or purifying a subpopulation of mRNAs, cDNA, or genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a composition of polynucleotide probes comprising first polynucleotide probes comprising at least a portion of
                                                                                                                                                                                                                                                                                                                         61 GCGCAACGNCGCCAACGCGCGAGAGCGGGCCCGCATGCGAGGCTTGAGGCCTTCT
                                                                                                                                                                                                                                    LysAlaProThrLysLysSerProLeuSerGlyValSerGln-GluGlyLysGlnValGl
                                                                                                                                                                                                                                                                G; 27 T; 0 U; 3 Other;
                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
        seqdata.uspto.gov/sequence.html?DocID=06500938B1
                                                                                                                                                                    Gaps:
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                                                                                                                                                                                                   US-09-701-674A-23 (1-179) x ACA56430
                                      72
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                                       55 A; 83 C;
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353.00
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10
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                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
                                      Sequence 240 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US2004010136-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                       Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L5-JAN-2004
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G; 27 T; 0 U; 3 Other;

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Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:

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The present invention describes a method (M1) for screening for an antinoplastic agent. The method involves exposing cells to a chemical agent to to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancinoma, neuronedocrine carcinoma, papillary carcinoma and Wilm's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carter KC, Ebner R, Endress G, Horrigan S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 3856; 44pp; English.
                                                                      2000US-0233133
2000US-0233617P
2000US-0234034P
2000US-0234052P
2000US-0234503P
2000US-0234503P
2000US-0234503P
2000US-0234503P
2000US-0234924P
2000US-0234924P
2000US-0235082P
2000US-0235082P
2000US-0235082P
2000US-0235082P
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2000US-0235638P.
2000US-0235711P.
2000US-0235720P.
2000US-0235840P.
2000US-0235863P.
2000US-0235863P.
2000US-0235863P.
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2000US-0236842P-
2000US-0231891P-
2000US-02317173P-
2000US-0237294P-
2000US-0237294P-
2000US-0237294P-
2000US-0237294P-
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2000US-0236109P.
2000US-0236111P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Young PE, Augustus M,
Soppet DR, Weaver Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AVAL-) AVALON PHARM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-188264/24.
                                                                                                  18-SEP-2000; 2
20-SEP-2000; 2
20-SEP-2000; 2
20-SEP-2000; 2
22-SEP-2000; 2
22-SEP-2000; 2
                                                                                                                                                                                                                                                         25-SEP-2000; 25-SEP-2000; 25-SEP-2000; 25-SEP-2000; 25-SEP-2000; 25-SEP-2000; 25-SEP-2000; 25-SEP-2000; 26-SEP-2000; 26-SE
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27-SEP-2000;
27-SEP-2000;
27-SEP-2000;
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02-OCT-2000;
02-OCT-2000;
02-OCT-2000;
02-OCT-2000;
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28-SEP-2000;
28-SEP-2000;
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27-SEP-2000;
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03-OCT-2000
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03-OCT-2000
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LysProGluSerAspLeuLysGluValValThrAlaSerArgLeuCysGlyThrThrAla 178
                                                                                                                                                                                                                                                                                                                                                                                                                                     LysTyrGluAsnGlyTyrIleHisProValAsnLeuThrTrpProPheMetValAlaGly 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122
                                                                                                                                                                                                                                                                                                                                                                              62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, cancer, colon, breast, ovary, oesophagus, kidney, thyroid, stomach, lung, prostate, pancreas; carcinoma, antitumour, cancerous; cytostatic, gene therapy, antineoplastic, Wilm's tumour, adenocarcinoma,
                                                                                                                                                                                                                                                                                                                        119 AspThrLeuArgLeuAlaSerSerTyrIleAlaHisLeuArgGlnIleLeuAlaAsnAsp
                                                                                                                                                                                                                                                                                                                                                        3 GACACGCTCAGGCTGGCGTCCAGCTACATCGCCCACTTGAGGCAGATCCTGGCTAACGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 AATACGAGAACGGGTACATTCACCCGGTCAACCTGACGTGGCCCTTTATGGTGGCCGGG
U; 7 Other;
                                                                             697
61
0
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                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
Sequence 697 BP; 190 A; 164 C; 156 G; 180 T; 0
                                                                                                                                                                                                                                                                       US-09-701-674A-23 (1-179) x ABL65519 (1-697)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABL65935 standard; DNA; 697 BP.
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2000US-023313P.

2000US-0233133P.

2000US-023340P.

2000US-0234609P.

2000US-0234509P.

2000US-023450P.

2000US-023450P.

2000US-023450P.

2000US-023450P.
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2000US-0235134P.
2000US-0235280P.
2000US-0235637P.
2000US-0235638P.
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                                                                                   92e-26
                                                                                                          318.00
100.00%
100.00%
34.68%
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                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
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18-SEP-2000;
18-SEP-2000;
20-SEP-2000;
20-SEP-2000;
20-SEP-2000;
22-SEP-2000;
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25-SEP-2000;
25-SEP-2000;
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                                                         Alignment Scores:
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27-SEP-2000;
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XXX ABL 65935

XXX ABL 6 ABL 6
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2000US-0235840P

27-SEP-2000;

123 AAACCCGAGAGTGACCTGAAAGAAGTGGTGACCGCGAGCCGCTTATGTGGAACCACGGG 182

Ser 179 TCC 185

179 183

159

LysProGluSerAspLeuLysGluValValThrAlaSerArgLeuCysGlyThrThrAla

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Human; benign prostatic hyperplasia; BPH; prostate cancer; gene;
                                                                                                                                                                                                            Human benign prostatic hyperplasia gene #679.
                                                                                                                                     ABK64784 standard; DNA; 697 BP.
                                                                                                                                                                                                                                                                                                                                                                  07-AUG-2000; 2000US-0223323P.
                                                                                                                                                                                                                                                                                                                                           07-AUG-2001; 2001WO-US024708.
                                                                                                                                                                                       18-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                        (GENE-) GENE LOGIC INC. (NISB ) JAPAN TOBACCO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Munger WE, Kulkarni P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-257476/30.
                                                                                                                                                                                                                                                                                         WO200212440-A2.
                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                   14-FEB-2002.
                                                                                                                                                               ABK64784;
                                                                                                              RESULT 14
                                                                                                                           ABK64784
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                                                                                   셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a method (MI) for screening for an antinoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in comprises a sequence (S) selected from 844° sequences (St. where (I) comprises a sequence (S) selected from 844° sequences (given in ABL61664 to ABL70110), or is at least 954 identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data oblected with respect to the anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adminesting ductal cancer, infiltrating ductal cancer, infiltrating ductal cancer, infiltrating ductal cancer, infiltrating cancer, infiltrating ductal cancer, infiltrating ductal cancer, infiltrating ductal cancer, infiltrating ductal cancer, infiltrating and Wilm's call.
                                                                                                                                                                                                                                                                                                                                                                              Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set.
                                                                                                                                                                                                                                                                                                                    Horrigan S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 697 BP; 190 A; 164 C; 156 G; 180 T; 0 U; 7 Other;
                                                                                                                                                                                                                                                                                                                    Ebner R, Endress G,
                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 4272; 44pp; English.
                                                                                                                                                                                                                                                                                                                    Carter KC,
                                                                                                           2000US-0237172P.
2000US-0237173P.
2000US-0237278P.
                                                                       2000US-0236111P.
2000US-0236842P.
2000US-0236891P.
                                               2000US-0236034P
2000US-0236109P
                                                                                                                                                            2000US-0237295P
2000US-0237316P
                                                                                                                                                  2000US-0237294P
                                                                                                                                                                                       2000US-0237425P
                                                                                                                                                                                                                                                                                                                 Augustus M,
Weaver Z;
                                                                                                                                                                                                                                                                                          (AVAL-) AVALON PHARM.
                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-188264/24.
                                             28-58P-2000;
28-58P-2000;
29-58P-2000;
29-58P-2000;
20-001-2000;
02-001-2000;
02-001-2000;
03-001-2000;
03-001-2000;
03-001-2000;
03-001-2000;
03-001-2000;
                                                                                                                                                                                                                          03-OCT-2000;
03-OCT-2000;
01-NOV-2000;
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Soppet DR,
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5

Yamamoto

Waga I,

Getzenberg RH,

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The invention relates to a method of diagnosing (1) the onset or progression of benign prostatic hyperplasia (BPH), or screening (II) for or indentifying an agent that modulates the onset or progression of BPH.

The method is based on changes in gene expression in BPH tissue isolated from patients exhibiting different clinical states of prostate class or progression for the screening of its comparises of prostate cells from the subject that are differentially regulated compared to normal prostate cells from the subject that are differentially regulated compared to normal prostate cells from the subject that are differentially regulated compared to normal prostate cells from the subject that are differentially regulated compared to normal prostate cells or BPH-like cell population, exposing the calls to the agent, preparing a second gene expression profile of the agent exposed cells, and comparing the first and second gene expression of BPH. (II) is useful confident or progression of BPH. (II) is useful for diagnosing the first or progression of BPH. (II) is useful cor in a tissue or cells, by comparing the expression level of expression in the database, and displaying the expression levels given in the generic and displaying the expression levels or expression level or expression level in the database, and displaying the expression levels or expression level in the database or cells to the leading BPH or progression the level in a tissue or expression for the restrict or expression level in the database, and displaying the expression levels or expression levels are useful for treating BPH or progression the level in a tissue or expression levels are useful for treating BPH or progression the level of the lead of the 
Identifying drugs for and diagnosing benign prostatic hyperplasia, by detecting expression levels of one or more genes in prostate cells fropatient that are differentially regulated compared to normal prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human benign prostatic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         697
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                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 367; 444pp; English.
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Pred. No.:
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LystyrgluðsnGlytyrileHisProValðsnLeuthrtrpProPheMetValðlagly 158

AspThrLeuArgleuAlaSerSerTyrIleAlaHisLeuArgGlnIleLeuAlaAsnAsp 138

697 00 00 00

Length:
Matches:
Conservative:
Mismatches:
Indels:

9.92e-26 318.00 100.00% 100.00% 34.68%

Similarity:

Query Match: Best Local

Percent Similarity:

Alignment Scores:

Gaps:

US-09-701-674A-23 (1-179) x ABL65935 (1-697)

119

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139 3

63

GACACGCTCAGGTGGCGTCCAGCTACATCGCCCACTTGAGGCAGATCCTGGCTAACGAC

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138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated polynucleotide comprising any one of determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide
                                                                                                                                                                 158
                                                                                                                                                                                          122
                                                                                                                                                                                                                    LysProGluSerAspLeuLysGluValValThrAlaSerArgLeuCysGlyThrThrAla 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA.
                                                                                                                                                                                                                                     123 AAACCCGAGAGTGACCTGAAAGAAGTGGTGACCGCGAGCCGCTTATGTGGAACCACCGCG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST; genome mapping; biodiversity; genetic disorder.
                                                                                                                                     62
                                                                                                                           GACACGCTCAGGCTGGCGTCCAGCTACATCGCCCACTTGAGGCAGATCCTGGCTAACGAC
                                                                                                          ASDThrLeuArgLeuAlaSerSerTyr1leAlaHisLeuArgGln11eLeuAlaAsnAsp
                                                                                                                                                                LysTyrGluAsnGlyTyrIleHisProValAsnLeuThrTrpProPheMetValAlaGly
                                                                                                                                                                                AATACGAGAACGGGTACATTCACCCGGTCAACTGAGCGTGGCCCTTTATGGTGGCCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jones LW
 40000
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 Matches:
Conservative:
Mismatches:
                                        Indels:
                                                     Gaps:
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                                                                                 US-09-701-674A-23 (1-179) x ABK64784 (1-697)
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                                                                                                                                                                                                                                                                                                                                                           ACH23969 standard; cDNA; 493 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Human adult ovary cDNA #2349
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318.00
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100.00%
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STACHE-CRAIN
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sequences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. The purified polypeptide is useful for generating antibodies specific for it. The present sequence is useful for generating antibodies specific for it. The present sequence is one of the 38043 isolated cONA/EST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at
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Db 1021 TATTAACTTCTACCGTGAATGACTCTGCTGCTGCTCGAGTGCAATGTAATT 1080  Qy 1081 ATAAATATAATAGATAAGACTTTGCTACCAGTGCAATGTGTAATT 1080  Db 1081 ATAAATATATAAATAGATAAGACCTATCAATGTTTTTGTACAATATGTTGTAAAAT 1140  Qy 1141 GTAGATCATAGGATAGCTGACTTTGACATTTTTTGTACAATATGTTGTAAAAT 1200  Db 1141 GTAGATCATAGGATAGCTGACTTTGACAGTTATAAAGTAATTCACTTAAAGATA 1200  Qy 1201 TATATTTTTTAAACAAGTTTTGCTACATTTTTGAAATAATTCACTTAATTGCTAA 1260  Db 1201 TATATTTTTTCAAACAAGTTTTGCTACTTTTGAAAATAATTCTTTAATTGCTAA 1260  Qy 1261 AAAAAAAAAAAA 1272  Db 1261 AAAAAAAAAAA 1272	RESULT 2 AF035718 LOCUS LOCUS DEFINITION Homo sapiens mesoderm-specific basic-helix-locp-helix protein (POD1) mRNA, complete cds. ACCESSION AF035718 VERSION AF035718.1 GI:2745886 KEYWORDS SOURCE Homo sapiens (human) ORGANISM Homo sapiens (human) MAMMMalia; Buteleostomi; Homomalia; Buteleostomi; Homomalia; Butheria; Prinates; Catarrhini; Hominidee; Homo.	theria; Primates; Catarrhini; Hominidae to 1254)  ", Vanden Heuvel, G.B. and Igarashi, P. soderm-specific basic-helix-loop-helix p. mal and glomerular epithelial cells in tl. (1-2), 37-48 (1998)  to 1254)  and Igarashi, P. desion (180)  24-NoV-1997) Internal Medicine, Yale Unitation (240)  cation/Qualifiers  1254	/organism="Homo sapiens" /mol Lype="hmRNA" /db xref="taxon:9606" /chromosome="6" 11254 /gene="POD1" /gene="POD1" /note="POD1" /product="mesoderm-specific basic-helix-loop-helix /product="mesoderm-specific basic-helix	/procedulary / procedulary / p
Query Match         100.0%;         Score 1272;         DB 6;         Length 1272;           Best Local Similarity 100.0%;         Pred. No. 7e-249;         O; Mismatches 0; Indels 0; Gaps 0;           Matches 1272;         Conservative 0; Mismatches 0; Indels 0; Gaps 0;           QY         1 TCTACGGCCACGACTCTGGGAAACAGAGAGCCGGTTCCTCTGCTGCAGAAGTC 60           Db         1 TCTACGGCACGACTCTGGGAAACAGAGAGCCGTTCTTGCTGCAGAAGTC 60           QY         61 TCGGGGTTCCTTCTCACAACTCTGCGAAAGAGTTGTGAGACCCAACCAA	24. CTCTCCCCCGTCCACCCCCAACATCTCCCCCCCCCCCCC		61 AGCAGATCCTGGCTAACGAGAACGGGTACATTCACCCGGTCAACCTGACG 61 AGCAGATCCTGGCTAACGACAAATACGAGAACGGGTACATTCACCCGGTCAACCTGACG 61 AGGCAGATCCTGGCTAACGACAAATACGAGAACGGGTACATTCACCCGGTCAACCTGACG 721 TGGCCCTTTATGGTGGCCGGGAAACCCGAGAGTGACCTGAAAGAAGTGGTGACCGCGGGC 721 TGCCCTTTATGGTGGCCGGGAAACCCGAGAGTGACCTGAAAGAAGTGGTGACCGCGGGC 781 CGCTTATGTGGAACCACCGCGTCCTTGAAGTGACTGAAAGAAGTGGTGACCGCGGGC 781 CGCTTATGTGGAACCACCGCGTCCTTGAACTTGAAGAAGTGGTGACGCGCTC 781 CGCTTATGTGGAACCACCGCGTCCTTGAACTTGGAGAAAGGGGGCGCTC 781 CGCTTATGTGGAAACCACCGCGTCCTTGAACGTGCGAGTTGCGGAAAGGGCGCCTC 781 CGCTTATGTGGAAACCACCGCGTCCTTGAACGTGCGAGTTGCGGAAAGGCGCGCTC 761 CGCTTATGTGGAAACCACCGCGTCCTTGAAGAGCGCGCTC	000   000

Oy 1088 TATAAATAGATAAGACCTATCAATGTATCTT  Db 1081 TATAAATAGATAAGACCTATCAATGTATCTT  Oy 1148 ATAGGATAGCTGACTTTGACAGTCACTTATAT  Db 1141 ATAGGATAGCTGACTTTGACAGTCACATTATAT  Oy 1208 TTTTCAACAGGTTTTGTGTGACTTTATATATATATATATA	RESULT 3 AP047419 LOCUS DEFINITION HOMO sapiens epicardin mRNA, compla ACCESSION AF047419 ACCESSION AF047419 VERSION KEWORDS SOURCE HOMO sapiens (human) ORGANISM Homo sapiens Eukeryota; Metazoa; Chordata; Cran Mammalia; Eutheria; Primates; Cata: REFERENCE I (bases 1 to 1257) AUTHORS Gilbert, D.J., Mifsud, L., Hartley, L., Bil Gilbert, D.J., Jonkins, N.A. and Har TITLE exploseed in epicardium, branchial of developing lung, gut, kidney, all Geveloping lung, gut, kidney, all MEDLINE PUBMED PUBMED REFERENCE 2 (bases 1 to 1257) AUTHORS RODALL. and Mifsud, L. TITLE PUBMED PUBMED PUBMED AUTHORS RODAL. and Mifsud, L. TITLE PUBMED PUBMED AUTHORS RODAL. and Mifsud, L. TITLE PUBMED AUTHORS RODAL. and Mifsud, L. TITLE PUBMED AUTHORS RODAL. and Mifsud, L. TITLE JOURNAL Builded AUTHORS RODAL. and Mifsud, L. TITLE JOURNAL SUBMISSION AUTHORS	Melbourne, VIC 3050, Australia Location/Qualifiers 11257 / organism="Homo sapiens" / mol type="mgMA" / db_Xref="taxon:9606" 260799="mgMA" / function="basic helix-loc" / note="expressed in embry/mesenchyme-derived tissues / function="basic helix-loc" / note="expressed in embry/mesenchyme-derived tissues / foodon_start=1 / product="epicardin" / protein id="AACG5322.1" / db_Xref="G1:2921853" / translation="MSTGSLSDVED] / kTYLPWVPPDTKLSKLDTLRRASSYY RSDLKEVVTARSLCGTTAS.	ORIGIN  Query Match Query Match Best Local Similarity 99.8\$; Pred. No. 7 Matches 1254; Conservative 0; Mismatcher Oy 9 CACGACTCTGGGAAACAGGAAACAGGAGCCG Db 1 CACGACTCTGGGAAACAGGAAACCGG Oy 69 TCCTTCTCACAGACTGGGAAACAGAGGCTG Oy 69 TCCTTCTCACAGACTGGGAAAGGGTGCGAACAGGGTGTGGGAAACAGAGGGTGCGGAACAGGGGTGCGGAACAGGGGTGCGGAACAGGGGTGCGGAACAGGGGTGCGAAGGGTGCGAAGGGTGCGAAGGGTGCGAAGGGTGCGAAGGGTGCGAAGGGTGCGAAGGGTGCGAAGGGTGCGAAGGGTGCGAAGGGTGCGAAGGGTGCGAAGGGTGCGAAGGGTGCGAAGGGTGGGAAAGGGTGCAAGGGTGGGAAAGGGTGAAGGGTGGGAAAGGGTGAAGGGTAAGGTGAAGGGTAAGGGTAAGGGTAAGGGTAAGGGTAAGGGTAAGGGTAAGGGTAAGGAAGGGAAAAGGGTAAGGGTAAGGGTAAGGGTAAGGGTAAGGGTAAGGGTAAGGGTAAGGGTAAGGGAAAGGGTAAGGAAGGGTAAGGGTAAGGGTAAGGGTAAGGGTAAGGGTAAGGGTAAGGGTAAGGGTAAGGGTAAGGAAGGGTAAGGGTAAGGGTAAGGGTAAGGGTAAGGGTAAGGGTAAGGGTAAGGGTAAGGGTAAGGAAGGGAAAGGGTAAGGGTAAGGGTAAGGGTAAGGGTAAGGGTAAGGGTAAGGGTAAGGGTAAGGAAGGGAAAGGGTAAGGAAGGGTAAGGAAGGGTAAGGAAGGGAAAGGGTAAGGAAGGGAAAGGAAGGAAGGGAAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGAAGGAAGGAAGGAAGGAAAA
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λΌ <sub>.</sub> qα	1148 ATAGGATAGCTGACTTTGACAGTCACATTTATAAAGTAATTCACTTAAAGATATATTTTTTTT	AGTAATTCACTTAAAGATATATATT 1207 
ò d	1208 TITICAAACAAGTITIGCTACTITIGAAAATAAAICTITCITIATAITGCTAAA 	TCTTTCTTATATTGCTAAA 1261 
RESULT 3 AF047419 LOCUS DEFINITION VERSION VERSION KEYWORDS SOURCE ORGANISM	AF047419 Homo saplens epicardin mRNA, c AF047419 AF047419.1 GI:2921852 Homo saplens (human) Homo saplens (human) Sukarvota: Metazoa: Chordata:	mENA linear PRI 06-OCT-1998 ete cds. iata: Vertebrata: Euteleostomi:
REFERENCE AUTHORS TITLE	Mammalia; Eutheria; Primates; Catar (bases 1 to 1257) THORS Robb,L., Mifsud,L., Hartley,L., Bik Gilbert,D.J., Jenkins,N.A. and Hark epicardin: A novel basic helix-loop expressed in epicardium, branchial	tor generation
JOURNAL MEDLINE PUBMED REFERENCE	OURNAL DEV. Dyn. 213 (1), 105-113 (1998) EDLINE 98401941 FUENCE 973105 FRENCE 2 (bases 1 to 1257) UTHORS Robb, L. and Mifsud, L.	Sept, bad date
TITLE JOURNAL FEATURES SOUX	TLE Direct Submission URNAL Submitted (10-FBS-1998) Haematology and Cancer, Walter and Hall Institute of Medical Research, PO Royal Melbourne Hosp Melbourne, VIC 3050, Australia  Location/Qualifiers  source 11257 /organism="Homo sapiens" /mol_type="mRNA"	and Cancer, Walter and Eliza PO Royal Melbourne Hospital,
Sign	W	-helix transcription factor" ic epicardium and of lung, gut, kidney, and
		/product="epicardin" /protein_id="AAG6233.1" /db_xref="GI:292183" /trānslation="MSTGSLSDVEDLQEVEMLECDGLKMDSNKEFVTSNESTEESSNC MSDSPGKAGGGGGRRRKAPPKKSPLSGVSQEGKQVQRNTANARERARMRVLSKAFSRL KTTLPWQPPDTKLSKLDTLALASSYIAHLRQILANDKYENGYIHPVNLTWPFMVAGKP ESDLKEVVTASRLCGTTAS"
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ò qa	9 CACGACTCTGGGAGAGGGGAAACAGAGGCGGTTCCTCTGCTGCAGAAGTCCTCGGGGT 	TCCTCTGCTGCAGAAGTCCTCGGGGT 68
S S	69 TCCTTCTCACAACTCTGCGAAGGGAAAGGGTTGTGAGACCCAACCAGCCCAACTCCA 	TGAGACCCAACACACACCCAACTCCA 128 
ð	129 GETCCCAGCAGGAGGTGGCTGCGCACACTCGGGAGGCTCTTGGTTTCAGGGTCTCTCT	AGGCCTCTTGGTTTCAGGGTCTCTCT 188

	REFERENCE 1 AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W. AUTHORS Kits, such as nucleic acid arrays, comprising a majority of TITLE Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof JOURNAL Patent: WO 02068579-A 3972 06-SEP-2002; PEATURES Location (NY) (US) FEATURES Location/Qualifiers //organism="Homo sapiens" //mol_type="unassigned DNA" //do_xref="taxon:9606"	Ouery Match  Query Match  Best Local Similarity 99.6%; Pred. No. 4.1e-240;  Matches 1254; Conservative 0; Mismatches 0; Indels 5; Gaps 2;  Matches 1254; Conservative 0; Mismatches 0; Indels 5; Gaps 2;  Qy CCGACTCTGGGAGTGGGGAAACAGAGGGCGTTCCTCTGCTGCAGAAGTCCTCTGGGGG 68	129 GCTCCCAGCAGGAGGTGGCTGCCACACTCGGAGGCCTCTTGGTTTCAGGGTCTCTCT 188	305 AAGAGGTGGAATGTTGGAATGTGGACGGTTGAAAATGGATTGGAACAAGGAATTTGTGA 301 AAGAGGTGGAAATGTTGGAATTGTGAACAAGGAATTTGTGA 301 AAGAGGTGGAAATGTTGAACAGGGTTTGAAAATGGATTTCGAACAAGGAATTTGTGA 302 CTTCCAACGAGAAGACGAGAGAGAGACTCCAACAAGAAATTGTGTGA 365 CTTCCAACGAGAAGAAGAAGACTCCAACTGCGAGAAATGGGTCTCCCCAGAAGGGCC 425 GCGGCGGCCTGGAGAAGAAGAAGAAGAGCCCCCAAAAAAAA	485 GCAGGAGGGAAGCCAGCGCAACGCGCAACGGGGAAGGCGGAGGCGGAGGCGGAGGCGGGAGGCGGAGGCGGAGGCGGAGGCGGGAGGCGGGAGGCGGGAGGCGGGAGGCGGGGGG
121 GCTCCCAGCAGGAGGTGGCAACATICGGGAGGCCTCTTGGTTTCAGGGTCTCTT 180  189 GTCTCTCTCTCACCCTCTTCCTGGCTTTCTCTGTCTCTCTC	369 CAACGAGGACCCCGAGGAGACTCCAACTGCGAAATGGGTCTCCCCAGAAGGGCCGGGG 428		729 TATGGTGGCGGGAACCCGAGAGTGACCTGAAAGAGTGGTGACCGCGAGCCGTTATG 788  721 TATGGTGGCCGGGAAACCCGAGAGTGCGCGAACAGAGTGGTGACCGCGAGCGGTTATG 780  722 TATGGTGGCCGCGAAACCCGAGAGTGCGAGAAGAGAGGCGCGCTTATG 780  733 TGGAACCACCGCGTCCTGACCTTGGAGGTGTGGGGAAAGGCGCGCTCCCGGGGG 848  734 TGGAACCACGCGTCCTGACCTTGGAGGTGCGGGTCTGGGAAAGGCGCGCTCCCGGGGG 840  849 AGCGGCCCCCGGGAAGGCGACCCTGCCCTCCAGTGCTCTGGTTCTGCTTCCCCCTCGC 908  841 AGCGGGCCCCCGGGAAGGCGAACCCTGCCCTCAGTGCTTCTGTTCTTGTTCCCCCTCGC 900  841 AGCGGGCCCCCGGGAAGGCGACCCCTGCCCTCAGTGCTTCTGTCTTCTGCTTCCCCCTCGC 900	909 AATGCTCCTCTCTCTCCCACCCGGGGAACACTTTACAACGACGAGGAGATTCGTTT 968	1089 ATAAATAGATAAGAGCCTATCAATGTACAATATGTACAATATGTAGAAATGTAGATCA 1148  1081 ATAAATAGATAAGAGCCTATCAATGTACTTTTGTACAATATGTTGTAAAATGTAGATCA 1140  1149 TAGGATAGCTGACTTTGACAGTCACTTTATAAAGTAATTCACTTAAAGATATATTTT 1208  1141 TAGGATAGCTGACTTTGACAGTCACATTTATAAAGTAATTCACTTAAAGATATATTTT 1200  1209 TTTCAAACAAGTTTTGCTACATTTGAAAATAAATCACTTTAAAAGATATATAT

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Contact: MGC help desk
Tissue procurement: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web sites http://www.nisc.nih.gov/
Contact: nisc mgo@nhgTi.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakealey,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
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McDowell,J., Pearson,R., Salantipop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,B.D.
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4507394.
                                                                                                                                                                                                                                                               Direct Submission
Submitted (06-MAR-2002) National Institutes of Health, Mammalian
Gene Collection (MCC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generachion and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Pred. No. 1.6e-154;
0; Mismatches 16;
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gene="TCF21"
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COMMENT
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I (bases 1 to 3231)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Morce, T., Max, S.I., Wang, J., Haich, F.,
Catalenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Boack, S.A., McEwan, P.J.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodersen, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Retteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Buckson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
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kidney Mech. Dev. 71 (1-2), 37-48 (1998) 98175875

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KTTLPWVPPDTKLSKLDTLRLASSYIAHLRQILANDKYENGYIHPVNLTWPFMVAGKP
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2 (bases 1 to 1240)
Quaggin, S.E., Vanden Heuvel, G.B. and Igarashi, P.
Direct Submission
Submitted (24-NOV-1997) Internal Medicine, Yale University, 333
Cedar Street, New Haven, CT 06520-8029, USA
Location/Qualifiers
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// gene="Pod1"

// note="Pod1"

// codon. start=1

// product="mesoderm-specific basic-helix-loop-helix
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61.0%; Score 776; DB 10;
Best Local Similarity 79.4%; Pred. No. 8.3e-148;
Matches 1020; Conservative 0; Mismatches 200;
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Abramson, R. D., Mullahy, S. J., Bosak, S. A., McEwan, P. J.,
McKernan, K. J., Malek, J. A., Gunaratne, P. H., Richards, S.,
Worley, K. C., Hale, S., Garcia, A. M., Gay, L. J., Hulyk, S. W.,
Villalon, D. K., Muzny, D. M., Sodergren, E. J., Lu, X., Gibbs, R. A.,
Fahey, J., Hellon, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A. C., Shevchenko, Y.,
Dlokson, M. C., Rodriguez, A. C., Grimwood, J., Schmutz, J. Myers, R. M.,
Butterfield, Y. S., Rzzywinski, M. I., Skalska, U., Smailus, D. E.,
Schnerch, A., Schein, J. E., Jones, S. J. and Marra, M. A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
D. Proc., Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: MGC help desk
Email: Gapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc.mgc@nhgri.nih.gov/
Contact: nisc.mgc@nhgri.nih.gov/
Contact: nisc.mgc@nhgri.nih.gov/
Contact: N. Ayele, K. Becktrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Lazic, P., Legaspi, R.,
Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
Tsurgeon, C., Vogt, J.L., Walker, M.A.,
Young, A., Zhang, L.-H. and Green, E.D.
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ENDLKEVVTANRLCGTTAS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (19-UTN-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="gynonyms: epc, Pod1, capsulin, epicardin, Pod-1"

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/db_xref="MGI:1202715"
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through the I.M.A.G.B. Consortium/KLNL at: http://image.llnl.gov
Series: IRAK Plate: 108 Row: p Column: 16.
Location/Qualifiers
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    ..1246
    /organism="Mus musculus"
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    /strain="FVB/N"

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Strausberg, R. L., Feingold, E. A., Grouse, L. H., Derge, J. G.,
Altschul, S. F., Zeeberg, B., Buetow, K. H., Schemen, C. M., Schuler, G. D.,
Altschul, S. F., Jordan, H., Moore, T., Max, S. I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A. A., Rubin, G. M., Hong, L.,
Stapleton, M., Soares, M. B., Bonaldo, M. F., Casavant, T. L.,
Scheetz, T. E., Brownstein, M. J., Usdin, T. B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S. S., Loquellano, N. A., Peters, G. J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTAACTTCTACCGTGAATGACTCTGCAAGCCTTGCTGGTCCAAGTGCAATATGTAATTAT 1082
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Hidai,H., Bardales,R., Goodwin,R., Quertermous,T. and Quertermous,B.E.
Cloning of capsulin, a basic helix-loop-helix factor expressed in progenitor cells of the pericardium and the coronary arteries Mech. Dev. 73 (1), 33-43 (1998)
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/db_xref="taxon:10090"

/db_ref="taxon:10090"

1.1217
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/product="hadas helix-loop-helix factor Corl"
/productid="Adas 4256.1"
/db_xref="G1:2613019"
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Quertermous, E. E., Hidai, H., Fadel, B.,
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Pred. No. 1.8e-144;
0; Mismatches 199;
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                                                                                                            Mus musculus (house mouse)
Mus musculus
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Eliza

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/product== epicardin"
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RASPOKGRGGIGKRRAPTKKSPLSGVSGRGVQRNAANARERARMRVLSKAFSRL
KTTLDWVPPDTKLSKLDTLALASSYIAHLRQILANDKYENGYIHPVNLTWPFMVAGKP
ENDLKEVVTANRLCGTTAS"
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         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
1 (bases 1 to 1202)
                                                    Robb,L., Mifsud,L., Hartley,L., Biben,C., Copeland,N.G.,
Gilbert,D.G., Jenkins,N.A. and Harvey,R.P.
epicardin: A novel basic helix-loop-helix transcription factor gen
expressed in epicardium, branchial arch myoblasts, and mesenchyme
of developing lung, gut, kidney, and gonads
Dev. Dpn. 213 (1), 105-113 (1998)
                                                                                                                                                                                                                and Eliza
Hospital,
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/function="basic helix-loop-helix transcription facto
//note="expressed in embryonic epicardium and
mesenchyme-derived tissues of lung, gut, kidney, and
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PO Royal Melbourne
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llarity 79.3%; Pred. No. 6.4e-143;
Conservative 0; Mismatches 195;
                                                                                                                                                                   (bases 1 to 1202)

Robb, L. and Mifsud, L.

Direct Submission

Submitted (10-FEB-1998) Haematology ar

Hall Institute of Medical Research, PC

Melbourne, VIC 3050, Australia

Location/Qualifiers
                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/mol_type="mRNA"
ferrain="Balb/c"
/db_xref="taxon:10090"
199-738
   musculus
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144 120 204 180

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requests: clonerequest@sanger.ac.uk  On Oct 1, 2000 this sequence version replaced gi:10186519.  During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.  The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:  EMBL, Sw., SWISSPROT, Tr., TREMBL, Wp., WORMPEP, Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at http://www.sanger.ac.uk/REPP/Chr6  IMDORTANT: This sequence is not the entire insert of clone RPI-373A10 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true right end of clone RPI-73H22 is at 25087 in this sequence. The true right end of clone RPI-662A9 is at 100 in this sequence. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequence is annotated repeats but not necessarily within known annotated repeats but not necessarily within known amounted before the library RPI-112 constructed by the group	RP11-373A10 is from the library RPCI-11.2 constructed by the group of Fieter de Jong. For further details see http://www.chori.org/bacpac/home.htm vBCTOR: pBACe3.6. org/bacpac/home.htm vBCTOR: pBACe3.6. org/bacpac/home.htm vBCTOR: pBACe3.6. organism="Homo sapiens"    Loadism="Homo sapiens"   John Companiens   John Co	repeat_region 28963155 //note="Allu"O repeat: matches 36295 of consensus" //note="MIR repeat: matches 28255 of consensus" //note="match: GSS: Em:AQ565803" repeat_region / note="match: GSS: Em:AQ565803" repeat_region / note="MITIB repeat: matches 3386 of consensus" repeat_region / note="MITIB repeat: matches 3386 of consensus" repeat_region / note="MITID repeat: matches 3386 of consensus" repeat_region / note="MITID repeat: matches 33487 of consensus" repeat_region / note="MITID repeat: matches 325487 of consensus" //note="MITID repeat: matches 25542749 of consensus" //note="MITID repeat: matches 25542749 of consensus"	misc_feature 63676702  misc_feature 64816770  repeat_region 64816770  repeat_region /note="MrTIF repeat: matches 1264 of consensus"  repeat_region /note="MrTIF repeat: matches 155259 of consensus"  repeat_region /note="L2 repeat: matches 19692509 of consensus"  repeat_region /note="Alusg repeat: matches 1298 of consensus"  /note="Alusg repeat: matches 1298 of consen
10	925 925 855 985 915 971 971 971	1031 GATAGGAGCCTAICAATGTGTATTTGTACAATGTGTAAAATGTGTAAAATGTGTAAATGTGTAAAATGTGTAAATGTGTAAAATGTGTAAAATGTGTAAAATGTGTAAAATGTGTAAAATGTGTAAAAATGTTTTTT	DEFINITION Human DNA sequence from clone RP11-373Al0 on chromosome 6. Contains ESTS, STSS, GSSS and CPG islands. Contains the TCF21 gene for transcription factor 21, complete sequence.  ACCESSION AL356109 GT:10443434 KEYWORDS HTG; CpG island; TCF21; transcription factor 21.  ORGANISM HTG; CpG island; TCF21; transcription factor 21.  SOURCE HTG; CpG island; TCF21; transcription factor 21.  MARMADISM PAL3CAS, Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Hominidae; Homo.  REFERENCE I (bases 1 to 25186) AUTHORS Wallis, J.  TITLE Direct Submission JOURNAL Submitted (15-DEC-2000) Sanger Centre, Hinxton, Cambridgeshire, CBIO 1SA, UK. B-mail enquiries: humquery@sanger.ac.uk Clone

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GTGACTTCCAACGAGAGCACCCGAGGAGGCTCCAACTGCGGAGAATGGGTCTCCCCCAGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTCGGGGGTTCCTTCTCACACTCTGCGAAGGGGAAAGGGTTGTGAGACCCAACCAGACCC
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                                                                                                                                                                                                                                         21400. .21807
/note="MER21B repeat: matches 324. .714 of consensus"
                                                                                                                                                                                                                   note≂"MER21B repeat: matches 274. .361 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3399. .23661
note="MLT1H repeat: matches 285. .547 of consensus"
                                                                            .2750 of consensus"
                                                                                                                                                                       .128 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="AluJb repeat: matches 1. .301 of consensus" 3961. .24243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="MLT1H repeat: matches 1. .286 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          matches 1. .505 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .212 of consensus"
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                                                                                                                        .207 of
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Pred. No. 1.4e-135;
0; Mismatches 3;
                                                                  /note="L2 repeat: matches 2675.
20892. .21097
/note="AluSq repeat: matches 1.
21164. .21277
                                                                                                                                                                  /note="MER21B repeat: matches 7.
21279, .21359
                                                                                                                                                                                                                                                                       complement (21885, .22328)
/note="match: GSS: Em:AQ416499"
complement (21975, .22377)
/note="match: GSS: Em:AQ005575"
22354. .22941
                                                                                                                                                                                                                                                                                                                                                                                 .2354. .22941
Note="match: GSS: Em:AQ486523"
22364. .23813
'note="match: GSS: Em:B82669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       match: STS: Em:G48886"
complement(22530. 23061)
/note="match: GSS: Em:AQ792775"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22898. .23051
/note="MIR repeat: matches 60.
23399. .23661
       complement (19114. .19339)
/note="match: STS: Em:G14783"
20263. .20325
/note="L2 repeat: matches 2677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (24819. .25186)
/note="match: STS: Em:G30455"
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/note="MLT1D repeat:
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Best Local Similarity 99.6%;
Matches 719; Conservative (
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/product="ba373A10.1 (transcription factor 21)"
//note="match: CDNAs: Em:AB009453 Em:AF036945 Em:AF029753
Em:AF035715 Em:AF047418 Em:AF035718 Em:AF029753
Em:AF035715 Em:AF04766154 Em:AF035718 Em:AF061752
Em:AF087035 Em:AF0660154 Em:AF108016 Em:M99367 Em:AF061752
Em:AB007959 Em:U18658
Em:AB007959 Em:U18658
Em:AA007050 Em:AA013640 Em:AA0130758 Em:AA080760 Em:AA1927658
Em:AA22321 Em:AA0135410 Em:AA013075 Em:AA080760 Em:AA1927658
Em:AA02321 Em:AA03540 Em:AA032055 Em:AA080760 Em:AA02814
Em:AA027032 Em:AA035365 Em:AA03803 Em:AA028148
Em:AA027032 Em:AA038365 Em:AA178060 Em:AA03802
Em:AA03822 Em:AA038365 Em:AA178060 Em:AA03803
Em:AA03822 Em:AA038365 Em:AA178060 Em:AA03803
Em:AA03802 Em:AA0380360 Em:AA171066 Em:AA038036
Em:AA027107 Em:AV11062 Em:AV11066 Em:AA038036
Em:AA027107 Em:AV11062 Em:AV36565 Em:AA341736
Em:AA02107 Em:AA031010 Em:AV310710 Em:AA1178188
Em:AA021107 Em:AA031010 Em:AA031072 Em:AA3410993 Em:AV351557
Em:AA218010 Em:AA031010 Em:AA3410993 Em:AA351557
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/product=bha37310.1 (transcription factor 21)"
/product=bha37310.1 (transcription factor 21)"
/db_xref="G1:1253960s" |
/db_xref="G0A:04360s" |
/db_xref="Swiss-Prot:043680" |
/translation="MSTGSLSDVEDLOEVEMLECDGLKMDSNKEFVTSNESTEESSNC
RTTLPWVPPDTKLSKLDTLKLASSYIAHLRQILANDKYENGYIHPVNLTWPFMVAGKP
ESDLKEVVTASRLCGTTAS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tr:P79782
                                                                                                                                                                                                                                                                                                                                                                                                                     /widence=not_experimental
13096. 13165

/note="15" Copies 2 mer tc 85% conserved"

join(13182. .13631,15497. .15586)

/gene="TCF21"

/note="TCF21"

/note="TCF21"

/ricy5946 Tr:043545 Tr:064124 Tr:073615 Sw:013562

Tr:091418 Tr:061100 Tr:094612 Tr:097481 Tr:097482

Tr:090149 Sw:p79920 Sw:060867 Sw:p24899 Tr:097486

Tr:0906080 Sw:p79920 Sw:060867 Sw:p24899 Tr:097466

Tr:090839 Tr:070483 Tr:0974A3 Tr:055300 Tr:061246

Tr:0908339 Tr:097469 Tr:P97831 Sw:091616 Sw:P79766
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//note="NERSA repeat: matches 1. .121 of consensus"
complement(19104. .19320)
/note="match: STS: Em:621594"
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note="MIR_repeat: matches 49. .156 of consensus"
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note=199 copies 2 mer ct 72% conserved"

1787. .1882

note="18 copies 2 mer ct 97% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="CpG island"
/evidence=not experimental
complement(15682, 16091)
/note="match: GSS: Em:AQ031468"
complement(15788, 16037)
/note="match: STS: Em:G15194"
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/note="match: GSS: Em:AL214858'
15337, .15744
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evidence=not_experimental
1326. .13636
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCTCTGTCCCACCCCGCGGGAACACTTTACAACGAGGGGGGAGTTCGTTTCCAAACCAGA
                                                                                               CGTCCTGACCTTGGAGGTGCGAGTCTGGGAAAGGCGCGCTCCCGGGGGGAANGCGCNCNCT
                                                                              481 AAGAGCCTATCAATGTATCTTTTGTACAATATGTTGTAAAATGTAGATCATAGGATAGCT
                                                                                                                                                                                                                               620 TGGACACGCTCAGCTCCAGCTACATCGCCCACTTGAGGCAGATCCTGGCTAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            680 ACAAATACGAGAACGGGTACATTCACCGGTCAACCTGACGTGGCCCTTTATGGTGGCCG
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                                             1099 AAGAGCCTATCAATGTATCTTTTGTACAATATGTTGTAAAATGTAGATCATAGGATAGGT
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Seguence 4272 from Patent WO0194629.
AX333763
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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                                                                                                                                                              13515 GACACCAAGCTCTCCAAGCTGGACACGCTCAGGCTGGCGTCCAGCTACATCGCCACTTG 13574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horrigan, S., Soppet, D.R. and Weaver, Z. Cancer gene determination and therapeutic screening using signature
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                   GACACCAAGCTCTCCAAGCTGGACACGCTCAGGCTGGCGTCCAGCTACATCGCCCACTTG
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                                                                541 ATGCGAGTGCTGAGCCTTCTCCAGACTCAAGACCACCTGCCCTGGCTGCCCCCC
                                                                                                                                                                                               AGGCAGATCCTGGCTAACGACAAATACGAGAAACGGGTACATTCACCCGGTCAACCTGACG
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95.1%; Pred. No. 4e-108;
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Avalon Pharmaceuticals (US)
Location/Qualifiers
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Sequence 3856 from Patent WO0194629.
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Homo sapiens
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www.rzpd.de/products/orfclones/
Conteat: Ina Rolfs
RZPD Deutsches Ressourcentrum fuer Genomforschung GmbH,
Reubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +40 30 32639 101
This Clone is available from RZPD;
content RZPD (customer.service@rzpd.de) for further information.
This CDS clone is a part of a collection of human full length
expression clones generated by RZPD.
This CDS has been cloned without stopcodon.
The CDS has been inserted into pDONR201 via a BP Clonase(TM)
Faction. Additional sequence has been added in front of the start
codon (ATG): att. ADADAA GCT GGC ACC CCT GGT CAC GCT
After the last codon additional sequence has been added: CCA
GCC GCA GCG Gin front of the 3' att site (AC CCA GCT TTC TT).
Compared to the reference sequence NM_003206 we did not find any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CR450293 S37 bp mRNA linear PRI 18-MAY-2004 Homo sapiens full open reading frame cDNA clone RZPD0834B11D for gene TCF21, transcription factor 21; complete cds; without
                                                                                                                          ATGACTCTGCAAGCCTTGCTGGTCCAAGTGCAATATGTAATTATAAATATAATAGAT 1098
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www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPD0834B111D RZPDLIB;
Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD LIB No.
                                                                                   420
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1 (Dases I to 537)

Ebert,L., Schick,M., Neubert,P., Schatten,R., Henze,S. and Korn,B. Cloning of human full open reading frames in Gateway(TM) system entry, vector (pDoNR201)
TCTCTGTCCCACCCCGCGAGAACACTTTACAACGACGAGGAGATTCGTTTCCAAACCAGA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 537)
Ebert, L., Schick, M., Neubert, P., Schatten, R., Henze, S. and Korn, B.
Direct Submission (18-10)
Submitted (18-MAY-2004) RZPD Deutsches Ressourcenzentrum fuer
Genomforschung GmbH, Im Neuenheimer Feld 580, D-69120 Heidelberg,
                                                                                                                                                                                                                                                                                                                                                GACTITICACAGICACATITIAIAAAGIAATITICACTIAAAGAIAIATATITITITICCAACA---
                                         GGAGATCAATTGTACTTACAAAGATTCCCATCTATTTAACTTTAACTTTCTACGGGA
                                                                   GGAGATCAATTGTACTTACAAAGATTCCCATCTATTAACTTTATTAACTTCTACGTGA
                                                                                                                                                                       AAGAGCCTATCAATGTATCTTTTGTACAATATATGTTGTAAAATGTAGATCATAGGATAGCT
                                                                                                                                                                                                                                                          481 AAGAGCCTATCAATGTATCTTTTGTACAATATGTTGTAAATGTAGATCATAGGATAGCT
                                                                                                                                                                                                                                                                                                                                                                                            amino acid exchanges.
Clone distribution: http://www.rzpd.de/products/orfclones/
Location/Qualifiers
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Full ORF shuttle clone, Gateway(TM), complete cds.
Homo sapiens (human)
Homo sapiens
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Unpublished
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/codon_start=1
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REASPOKAGGGLGKRRKAPTKKSPLGGVSQEGKQVQRNAANARERAARRVLSKAFSRL
KTTLPWVPPDTKLSKLDTLRLASSYIAHLRQILANDKYENGYIHPVNLTWPFWVAGKP
ESDLKRVTAASRLGGTTAS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          421 GAGAACGGGTACATTCACCCGGTCAACCTGACGTGGCCCTTTATGGTGGCCGGGAAACCC
                                                                                                                                  'note="Vector: pDONR201, Site_1: attP1; Site_2: attP2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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larity 100.0%; Pred. No. 3.6e-99;
Conservative 0; Mismatches 0;
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